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April 7, 2006, 20:22:24 ; Search time 6020 Seconds (without alignments) 10622.738 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                               5883141 segs, 28421725653 residues
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Maximum Match 100%
Listing first 45 summaries
                                             OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1: gb ba:*

2: gb_in:*

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9: gb_pat:*

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                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | AB027428 Oryza sat | AK104862 Oryza sat | AX653028 Sequence | AF001523 Musa acum | AX006978 Sequence | AF112967 Triticum | Continuation (414 | AP004031 Oryza sat | Z22874 T.aestivum | AF004838 Musa acum | AK070677 Oryza sat | U72251 Oryza sativ | BD080855 Banana pr | AY612193 Hordeum v | Z22873 T.aestivum | Z15131 A. sativa mR | X52572 Barley DNA | X56260 Barley DNA |
|------------|-----------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|---------------------|-------------------|-------------------|
| SUMMARIES | QI | AB027428 | AK104862 | AX653028 | AF001523 | AX006978 | AF112967 | AP008207 413 | AP004031 | TABETGLUB | AF004838 | AK070677 | OSU72251 | BD080855 | AY612193 | TABETGLUA | ASBGLUCAN | HVBDG | HVGLUEND |
| | 8 | 15 | 15 | 9 | 15 | v | 15 | 15 | 12 | 15 | 15 | 15 | 15 | ø | 15 | 15 | 15 | 15 | 15 |
| | Match Length DB | 1280 | 1296 | 993 | 1141 | 1261 | 1439 | 110000 | 164394 | 1426 | 1041 | 1295 | 1834 | 3559 | 1249 | 1434 | 1448 | 6260 | 4643 |
| * Query | Match | 38.3 | 38.3 | 38.3 | 38.3 | 38.2 | 38.0 | 3766 | 37.6 | 37.5 | 37.5 | 37.3 | 37.2 | 36.9 | 36.4 | 35.0 | 35.0 | 34.0 | 33.8 |
| | Score | 431.4 | 431.4 | 431.2 | 430.6 | 430 | 427.2 | 423.2 | 423.2 | 422 | 421.8 | 419.4 | 418.2 | 415.6 | 409.8 | 394.2 | 393.6 | 382.4 | 380.8 |
| Result | No. | т | 7 | m | 4 | ហ | φ | 7 | œ | σ'n | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |

| X56775 H.vulgare G M62740 Hordeum vul | | AF112965 Triticum | AY353062 Vitis rip | M13237 Barley beta | S82315 PRm 6b=1,3- | AK060867 Oryza gat | AF323610 Oryza sat | AY768944 Oryza sat | AK121825 Oryza sat | M91814 Barley beta | AF239617 Vitis vin | AF515785 Hordeum v | M62907 H.vulgare L | A37992 Sequence 11 | AR037575 Sequence | AR164399 Sequence | I75201 Sequence 11 | AX653237 Sequence | AK068247 Oryza sat | AJ271367 Hordeum v | Y18212 Triticum ae | AK105972 Oryza sat | M23548 Hordeum vul | Continuation (180 | AC108874 Oryza sat |
|--|-------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| 5 HVGLB1 5 BLYGLB2 | | | | | 5 S82315 | · | 5 AF323610 | | 5 AK121825 | | 5 AF239617 | | 5 BLYCBGL32 | A37992 | AR037575 | AR164399 | 175201 | AX653237 | | _ | 5 TAY18212 | 5 AK105972 | 5 BLYGEH | 5 AP008211 179 | 5 AC108874 |
| 4849 1 5159 1 | - | - | - | - | ٦ | - | ٦ | _ | - | Н | ч | - | - | 1235 6 | 1235 6 | 1235 6 | 1235 6 | 9 666 | - | ٢ | - | 7 | 1250 1 | - | 121293 19 |
| 33.8 | 32.9 | 32.7 | 32.4 | 32.0 | 31.8 | 31.4 | 31.3 | 31.3 | 31.3 | 31.3 | 31.3 | 30.9 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.5 | 30.5 | 30.5 | 30.4 | 30.4 | 30.4 | · | 30.3 |
| 380.8 378.6 | 370.2 | 368.2 | 364.8 | 360 | 357.6 | 353.8 | 352.2 | 352.2 | 352.2 | 352 | 351.6 | 347.8 | 346.2 | 346.2 | 346.2 | 346.2 | 346.2 | 343.4 | 343.4 | 343 | 342.2 | 341.8 | 341.6 | 340.4 | 340.4 |
| 19 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 4 | c 45 |

ALIGNMENTS

RESULT 1

| AB027428 | |
|------------|--|
| LOCUS | AB027428 1280 bp mRNA linear PLN 21-MAY-1999 |
| DEFINITION | a mRNA for beta 1,3-glucanase, complete cds, |
| | clone: E1149. |
| ACCESSION | AB027428 |
| VERSION | AB027428.1 GI:4884525 |
| KEYWORDS | beta 1,3-glucanase. |
| SOURCE | Oryza Bativa |
| ORGANISM | Oryza Bativa |
| | Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
| | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; |
| | Ehrhartoideae; Oryzeae; Oryza. |
| REFERENCE | 1 (bases 1 to 1280) |
| AUTHORS | Itoh, Y. and Sasaki, T. |
| TITLE | Oryza sativa mRNA for beta 1,3-glucanase |
| JOURNAL | Published Only in DataBase (1999) |
| REFERENCE | 2 (bases 1 to 1280) |
| AUTHORS | Itoh, Y. and Sasaki, T. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (17-MAY-1999) Yoshifumi Itoh, National Food Research |
| | Institute, Applied Microbiology; Kannondai 2-1-2, Tsukuba, Ibaraki |
| | 305-8642, Japan (E-mail:yosifumi@nfri.affrc.go.ib. |
| | Tel:+81-298-38-8075, Fax:+81-298-38-7996) |
| PEATURES | Location/Qualifiers |
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| | VVQLYKSNGIDSMRIYFPRSDILQALSGSSIALTMDVGNDQLGSLASDPSAAAFVQN |
| | NIQAFFGVNFKITTVGNEVSGGDTQNILFAMQNMNSALSAAGLGNIKVSTSVSQGVTA |

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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satch, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahady, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequenching & Analysis Group: Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Rugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Kusumegi, T., Kodama, T., Kawamata, M., Yokomizo, S., Niikura, J., Ikda, R., Ishibiki, J., Kawamata, M., Yokomizo, S., Niikura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Natsubara, K., Riken, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Shibara, K., Ishibiki, M., Hayatsu, N., Imotanik, Y., Itoh, M., Kagawa, I., Kondo, S., Komno, H., Miyazaki, A., Osato, N., Osta, Y., Saito, R., Saski, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ladachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fuyuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayateu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Horis, I., Ishibiki, J. Ishili, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kayamata, M., Kinchi, S., Kishikawa, Hirozame, T., Kishimoto, N., Kobayashi, M., Kodam, T., Kojima, K., Kojima, Y., Muura, J., Miyazaki, A., Masuda, H., Matsupama, T., Muura, J., Miyazaki, A., Masuda, H., Matsupama, T., Muura, J., Miyazaki, A., Mizuno, K., Murata, M., Nagata, T., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Nomura, K., Sakai, K., Sakai, D., Saka, J., Sakai, D., Sakai, D., Sakai, D., Sakai, D., Sato, K., Satoh, K., Tagama, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                       AKLU4862 1296 Dp mRNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone:001-043-E09, full
insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK104862.1 GI:32990071
FLI_CDNA; oligo capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
          ACCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAATAAC
                                                   971 ACCTACATTTTCGCCATGTTCAACGAGAACCAGAAGGGAGGCGACGACGAGAGGGCAC
                                                                                                       TITGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTCACTTGAGAAATT
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KEYWORDS
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ORGANISM
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VQDGGNAYQNLFDAIVDTFYSALESAGAGSVPIVVSESGWPSAGGTAASAGNAQTYNQ
NLINHVGQGTPKRPGSIETYIFAMFNENQKGGDETERHFGLFNPDQSPAYSINF"
NLINT. .1181
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                                                                                                                                                                                                                                 DB 15; Length 1280;
                                                                                                                                                                                                                           38.3%; Score 431.4; DB 15;
66.8%; Pred. No. 3.4e-75;
tive 0; Mismatches 321;
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           AACCAGAACCTGATCAACCACGTCGGGCAGGGGACGCCCAAGAGGGCCCCGGGAGCATCGAG 983
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                     rice. F.
URL. http://cdhaol.dna.affrc.go.jp/cDNA/
NIAS Rice Pull-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,B., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
PAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:8kikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
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On Oct 20, 1999 this sequence version replaced gi:2586138.
                                                                                                                                                                                                                                          May, G.D.,
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NY 14853, USA
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                                                                                                                                                                                                                                        Zhang, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1141;
                                                                                                                                                                                                                                      Peumans, W.J., Barre, A., Derycke, V., Rouge, P., Zhang, W., Delcour, J.A., Van Leuven, F. and Van Damme, E.J. Purification, characterization and structural analysis abundant bear1, 3-glucanase from banana fruit Eur. J. Biochem. 267 (4), 1188-1195 (2000)
                                                                                                                                                                      banana fruit
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                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (29-APR-1997) Plants and Human Health,
Institute for Plant Research, Tower Rd., Ithaca,
4 (bases 1 to 1141)
Van Damme, B.J., May, G.D. and Clendennen, S.K.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 430.6; DB 15;
Pred. No. 4.8e-75;
0; Mismatches 329;
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(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'organism="Musa acuminata"
                                                                                                                                   (bases 1 to 1141)
Clendennen, S.K. and May, G.D.
Differential gene expression in
Plant Physiol. 115 (2), 463-469
                                                                                                   Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                          3 (bases 1 to 1141)
Clendennen, S.K. and May, G.D.
                                                                   Musa acuminata
Eukaryota, Viridiplantae,
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PLN 21-MAR-2000

AF001523 1141 bp mRNA linear PLN Musa acuminata beta-1, 3-glucananse mRNA, complete cds.

RESULT 4 AF001523 LOCUS DEFINITION

1. .1261 /organism="Elaeis guineensis" /mol-type="unassigned DNA" /db xref="taxon:51953" /noFe="oil palm"

Patent: WO 0001804-A 2 13-JAN-2000; UNILEVER PLC (GB); UNILEVER NV (NL) Location/Qualifiers

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Length 1261;
Score 430; DB 6; Length 12
Pred. No. 6.4e-75;
0; Mismatches 350; Indels
38.2%;
                                                                  Matches 692; Conservative
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PAT 06-SEP-2000

linear

DNA

AX006978 1261 bp Sequence 2 from Patent W00001804 AX006978: GI:9994967 AX006978:1 GI:9994967

RESULT 5
AX006978
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
CETWORDS
SOURCE
ORGANISM

Elaeis guineensis (African oil palm) Elaeis guineensis Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Arecaceae, Arecoideae, Cocoeae, Elaeidinae, Elaeis.

Stratford, R. and Kemp, R. Nucleotide sequence

REFERENCE AUTHORS TITLE ø

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SEVVQLYGSNGITGMR!XFPADNEVGYQGGDTGSIIDL!IDVANEDLASLASDRAAATAWV
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                                                                                                         ATIGA#CAAAACTTTGGACTGTTTTTACCCAAATATGCAACCAGTCTACCCAATGAACTTT 1041
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1 (bases 1 to 1439)
Li,W., Faris,J.D., Muthukrishnan,S., Liu,D., Chen,P. and Gill,B.S. Isolation and Characterization of cDNA Clones of Acidic Chitinases and beta-1,3-Glucanases from Wheat Spike Induced by Fusarium
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2 (bases 1 to 1439)
Li,W., Faris,J.D., Muthukrishnan,S., Liu,D., Chen,P. and Gill,B.S. Direct Submission
Submitted (11-DEC-1998) Department of Plant Pathology, Kansas Stat. University, St. Claflin, Manhattan, KS 66506-5502, USA
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                                    --GGCGATTGAGACCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCAAGGG
                                                                                ATTGAGAATAACTTTGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTC
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Pred. No. 2.3e-74;
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/protein id="AAD28734.1"
/db_xref="GI:4741850"
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mol type="mRNA"
cultivar="Sumai 3"
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/chromosome="3A, 3B, 3D"
/clone="SMS38"
/tissue_type="spikelet"
/dev stage="adult"
1. .1439
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Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,
Katayose, Y., Wu, J., Nlimura, Y., Cheng, Z., Nagamura, Y.,
Antonio, B.A., Kanamori, H., Hoskawa, S., Masukawa, M., Arikawa, K.,
Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Arita, K.,
Hamada, M., Harada, C., Hijishita, S., Honda, M., Ichikawa, Y.,
Idonuma, A., Iijima, M., Ikeda, M., Ikeno, M., Ito, S., Ito, T., Ito, T.,
Ito, Y., Iwabuch, A., Kamiya, K., Karasawa, W., Katagiri, S.,
Kikuta, A., Kobayashi, N., Kono, I., Machita, K., Machara, T.,
Mizuno, H., Mizubayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M.,
Nakama, Y., Nakamichi, Y., Nakamura, M., Namiki, N., Negishi, M.,
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                     39901 TCCGGCGGCACACGCAGAACATCCTCCCGGCCATGCAGAACATGAACAGGCGCCCTCTCC
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                                                                  TCTGCCGGCCTTCAGAACATCAAGGTCTCCACATCAGTCTCCTTCGGCGTCGTCGTACC
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AP004031 BA000010
AP004031.3 GI:18844943
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|db_xref="GI:57900002"
|translation="MIQAARRVVAREHRNSIRQLVVRVNTPIYGYVINSAMSSRVIDP
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/bx xref="G1:57980003"
/translation="hypothemsprakessalthecsdhcidartheprdscalaigr
Rekregaacgegrywaarrenesregekcgvgvavaargwdvallggarlaaa
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RREALPSSGGDGGEHTASDGSSRGGAMTMPDCAGRDHSGLGPGKRKKRRRPRSFSRVL
RTLOLSKCLANNGGGETEGROWRGGDAGOARONITAAATGRSATTACARGKQRTARRR
GRRRRAAAKAEGAHTGAAHAHARAAHGQSGG"
Complement (20617. . 22531)
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//gene="pod/32003.6"
join(14)140. .19534,19628. .19798,20131. .>20327)
/gene="pod/32003.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted by GENSCAN
this category is not included in IRGSP standard"
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/gene="P0432C03.7"
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complement(join(20617. .20781,22514. .22531))
                                      'note="start and end point are not identified"
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complement (join (16784. .16957,17074. .17136))
/gence="P043CC3.5"
/gence="P043CC3.5"
/gence="P043CC3.5"
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join(<9579. .9608,9778. .9945,10345. .>10536)
gene="P0432C03.4"
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complement(join(6675. .6822,7790. .7845))
/gene="P0432C03.3"
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/protein id="BAD87985.1"
db_xref="GI:57900004"
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                                                                                                                                                   /codon_start=1
/product="hypothetical_protein"
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protein_id="BAB85416.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="hypothetical ORF
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predicted by GlimmerM
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/gene="P0432C03.8"
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Direct Submission

Direct Submission

Burbaitteed (08-AUG-2010) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki, 305-8602. Japan

(E-mail:teasaki@nias.affrc.go.jp, URLihttp://rgp.dna.affrc.go.jp/, Tel:81-298-38-441, Pax:81-298-38-4468)

On Feb 20, 2002 this sequence version replaced gi:16191730.

Genes were predicted from the integrated results of the following: GENSCAN (http://com.on/p.com/), Geneswark.hmm

(http://www.igr.org/tch/gilmmerm/gilmr.form.html), FGENESH

(http://www.igr.org/tch/gilmmerm/gilmr.form.html), RiceHPW

(http://www.igr.org/tch/gilmmerm/gilmr.form.html), gap2

(http://www.igr.org/software/gilmmerm/gilmr.form.html), gap2

(http://gilmin.cs.pun.edu/html/docs/simf.html), gap2

(http://gilmin.cs.pun.edu/html/docs/simf.html), gap3

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(http://gilmin.cs.pun.edu/html/docs/simf.html), gap4

(http://gilmin.cs.pun.edu/html/docs/simf.html), gap4

genomic sequence was searched against NCBI NonRedundant Protein database

with Bla57F ESTS represent the identified cDNA sequences using

Bla57N with the corresponding DBJ3 accession no.

Agene with identity or significant homology to a protein is

classified based on the protein but with full-length cDNA or EST homology to any protein but with full-length cDNA or EST homology to any protein but with full-length of partial galmost the enquence.

EST homology (covering almost the enti
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/gene="P0432C03.1"
complement (join(<1887. .2097,2212. .2402,2435. .>2491))
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complement(join(1887. .2097,2212. .2402,2435. .2491))
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/chromosome="1"
/chromosome="1"
Yano,M., Jiang,J. and Gojobori,T.
The genome sequence and structure of rice chromosome 1
Nature 420 (6913), 312-316 (2002)
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/codon_start=1
                                                                                                                                        Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission
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/gene="P0432C03.2"
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                                                                                                             REFERENCE
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                                                                                                                                                                                                                                                                                                                                              COMMENT
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31682 GTGGTGCAGGACGCGCGAACGCGTACCAGAACCTGTTCGACGCCATCGTCGACACGTTC 31741
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/codon_start=1
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/product="(1,3;1,4) beta glucanase"
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/db_xxef="GOA:070LM"
/db_xxef="GOA:070LM"
/db_xxef="InterPro::PR000490"
/db_xx
                                                                                                                                                                                                                                                                                                                                         31802 TGGCCGTCGGCCGGCGGCGCGGCGGCGCCGCAACGCGCAGACGTACAACCAGAAC 31861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31862 CTGATCAACCACGTCGGGCAGGGGCCCAAGAGGCCCGGGAGCATCGAGACCTACATT 31921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31922 TTCGCCATGTTCAACGAGAACCAGAAGGGAGGCGACGAGACGGAGAGGGCACTTCGGCCTC 31981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T.aestivum (1,3;1,4) beta glucanase mRNA, complete CDS. 222874
                                                                                                                                                                                                     31742 TACTCCGCGCTGGAGAGCGCCGGGGCCCGGGAGCGTCCCGATCTCGTGTCGGAGAGCGGG 31801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum (12.02. m.o.c.)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bopermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

1 (bases 1 to 1426)

1 (bases 1 to 1426)

1 (lai, D.M., Hoj, P.B. and Fincher, G.B.

Purification and characterization of (1-->3, 1-->4)-beta-glucan endobydrolases from garminated wheat (Triticum aestivum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            972
      GTCGTACAGGACGGGTCCTACGGTTACAACAACCTCTTCGATGCCATGGTCGACGCATTG
                                                                                                                                          TACTCGGCCCTGGAGAGCGCCGGAGGCCGAATGTCCCTGTTGTCGTGTCGGAGAGTGGC
                                                                                                                                                                                                                                                                           TGGCCGTCAGCGGGGGGCGCGCGCGCGTGTCTAATGCGCAGACTTACAATTCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITIGCCATGITCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAATAACTTTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                           TTGATCAACCATGTGGGTCAGGGGACGCCGAAGAGGCCAGGGGGGGATTGAGACCTACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-JUN-1993) Fincher G. B., University of Adelaide, Waite Campus, Plant Science, Glen Osmond, South Australia, Australia, 5064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TICAACCGGACCAGTCGCCGCATACTCCATCTAAGAAGATTGTT 32033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITIACCCIAACGAACAGCCIGICIATICGAICAGCIICACIIGAGAAAITI 1024
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/organism="Triticum aestivum"
/mol type="mRNA"
/strāin="Millewa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1,3; 1,4) beta glucanase.
Triticum aestivum (bread wheat)
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/chromosome="group 1"
/clone="lambda LW1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51. .1055
/EC_number="3.2.1.73"
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KEYWORDS
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TABETGLUB
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31097 ACAGTGCTGCAATCTATCGGCGTGTGCTACGGGGTGATCGGGAACAACCTGCCGTCGCCG 31156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31157 AGGGACGTCGTGCAGCTCTACAAGTCCAACGGCATCGACTCCATGCGCATCTACTTCCCA 31216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31217 AGAAGCGACATCCTCCAGGCCCTCAGCGCTCAAGCATCGCCCTCACGAGGTCGGC 31276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="MarmealGDKagardggggrssaaqkhrwgvgggggatslvagg
GVGAEDVEICWERKVVVPRPWHSPSSPHAHCREGECSSSSFASSKSKSLSLYCLLLLL
PPAFLEPADHRWSTVTCFDSAAVGVG"
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mvvraggppstnalilafvlplslfvgtlitaarvaddlderplremesnkalmeene
Dfeqdggeebeeedaeqpapvekegvlvaaaprtrnrpkrevq"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31394 receseceseacadecadaaacarecreceesecarecadaacareaaceceeeeeee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
gene="P0432C03.8"
note="supported by full-length cDNA(s): AK070587"
join(27245. 27514,27616. .27783)
gene="P0432C03.8"
note="contains full-length cDNA(s): AK070587"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 164394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c29103. .>29489
'gene="P0432C03.9"
'note="start and end point are not identified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 423.2; DB 15; Length
Pred. No. 1.5e-73;
0; Mismatches 293; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29103. .29489
/gene="P0432C03.9"
/note="predicted by GlimmerM etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(30499. .30670,31101. .32225)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="hypothetical protein"
protein id="BAD87987.1"
db_xref="G1:5790006"
                                                                                                                                                                      /codon_start=1
/product="unknown_protein"
                                                                                                                                                                                                                                     /protein_id="BAD87986.1"
'\'\db xref="GI:57900005"
                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="P0432C03.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                           .29489
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al Similarity 67.6%;
644; Conservative
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/trainiation="Lyavptryosigocygmicannippessyvslyksnniarmrlyd
Pnoaaloalrnsniovildvprsdvoslasnpsaagdwirrnvaywpsvsfryiavo
nelifosdiaoyiilpamrniynalssaglomoircystavtototofysppesaafssa
Aqaylspivdpayranyavpypsyrsytonpogislpyalftascovvqdgrfsyg
Nlfdaivdaypraaraychvavypsesogmpsaaggaraasysnaoyinqniirhygg
Gtprrpgkeirayifemfnenokaagieqnpsqclfpypnkopvygisp"
                                                                                                                                     1005 TGGGGACTCTTCTACCCCAACATGCAGCACGTCTACCCCATCAGCTTCTGATGAGCTAGC 1064
                                                                           PLN 18-NOV-1999
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1; Zingiberales; Musaceae;
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Submitted (20-MAY-1997) Horticulture, National Taiwan University,
No.1 Section 4 Roosevelt Road, Taipei, Taiwan 10617, Republic of
China
                                                                                                                    TTTGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTCACTTGAGAAATT
                               AACCAGTACCTCATCAACCACGTCGGGCGCGCGCCCCCCGCCCACCCGGGCGCCCATCGAG
                                                            ACCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAATAAC
    AATTCCAATTTGATCAACCATGTGGGTCAGGGGACGCCGAAGAGGCCCAGGGGCGATTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                            Chen.Y.-C., Do,Y.-Y. and Huang,P.-L.
Chen.Y.-C., Do,Y.-Y. and Huang,P.-L.
Isolation and nucleotide sequence of a fruit ripening-related encoding glucan endo-1,3-beta-glucosidase homolog from banana (Accession No. AF004838) (FGR97-151)
Plant Physiol. 115 (2), 864 (1997)
Huang,P.
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Pred. No. 2.7e-73;
0; Mismatches 297; Indels 18;
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Musa acuminata beta-1,3-glucanase mRNA, partial cds.
AF004838
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Spermatophyta, Magnoliophyta, Liliopsida,
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/b zrain="Hsien Jin Chiao"
/db zrae="taxon:4641"
/clone="pBGL1"
/tissue_type="fruit peel"
/dev grage="tipening stage 3"
/note="AAA genome"
/l. 970
/codon start=2
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/protein_id="AAF08679.1"
/db_xref="GI:6448757"
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/organism="Musa acuminata"
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37.5%;
Best Local Similarity 68.3%;
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Musa acuminata
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135. .1052
135. .1052

" product="(1,3;1,4) beta glucanase"
/EC_number="3.2.1.73"
/Function="cell wall metabolism"
/evidence=experimental
1053. .1426
                                                                                                                                                                               37.5%; Score 64.7%; Pred. No. 2.5e-... 0; Mismatches 355;
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nes 661; Conservative
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satch, K., Magata, T., Kawagasahira, N. Doi, K., Kikhimoto, N., Yazaki, J. Ishikwaa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Conneda, B., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shimiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Irda, R., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuma, M., Yoshimura, A., Miura, J., Kawai, J., Carninci, P., Adachi, J., Alzawa, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Alzawa, K., Rakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayasuki, M., Miyazaki, A., Caraininci, P., Adachi, J., Sato, K., Shibata, K., Shinagawa, T., Futoh, M., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y., Collection, mapping, and annotation of over 28,000 cDNA clones from collection, appling, and annotation of over 28,000 cDNA clones from
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Pujimura,T., Fukuda,K., Hanagaki,T., Hara,A., Hashizume,W., Pujimura,T., Fukuda,K., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hizamoto,K., Hiraoka,T., Hori,P., Hotta,I., Iida,J., Iida,Y., Ishikawa,M., Itoth,M., Kagawa,I., Kanagwa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa,Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,Y., Kojima,Y., Kojima,Y., Kojima,Y., Kojima,Y., Kojima,Y., Miura,J., Miyra,J., Miyra,M., Masuda,H., Matsuvama,T., Miura,J., Miyrazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namaski,T., Narikawa,R., Nikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sujiyama,A., Suzuki,Y., Sasaki,D., Sato,K., Satoh,K., Sasaki,T., Tagama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
                Oryza sativa (japonica cultivar-group)
sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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(bases 1 to 1295)

12869764

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URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Obneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAIRS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Rujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Natsubara,K. and Murakami,K., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.,
and Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Yoshimura, A.

Direct Submission

Talis1-29-838-7007, Fax.

This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                          rice.
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oryza sativa (japonica cultivar-group) cDNA clone:J023063017, full insert sequence.

DEFINITION RESULT 11 AK070677

ACCESSION VERSION KEYWORDS SOURCE

AK070677.1 GI:32980701 FLI_CDNA; CAP trapper. Oryza sativa (japonica cultivar-group)

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Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Yasunishi, A. and Hayashizaki, Y.
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/mol type="mRNA"
/cultivar="wipponbare"
/db xf=taxon:39947"
/clone="J023063017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 15; Length 1295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 8.1e-73;
0; Mismatches 321; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGCAGCTCAGCACATCACCATGGCTGCCATGGCATCCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 419.4;
Pred. No. 8.1
                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 681; Conservative
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                                                                                                                                                                                                    ACCTACATTTTCGCCATGTTCAACGAGAACCAGAAGGGAGGCGACGAGACGGAGAGGGCAC 1042
                                                                                                                                                                                                                                                                    1043 TTCGGCCTCTTCAACCCGGACCAGTCGCCGGCATACTCCATCAATTTCTAAGAAGATGT 1102
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Romero, G.O., Simmons, C.R. and Rodriguez, R.L.

Direct Submission

Submitted (24-SRP-1996) Molecular and Cellular Biology, University of California at Davis, CA 95616, USA

Location/Qualifiers
  843
                                        922
                                                                              903
                                                                                                                   AACCAGAACCTGATCAACCACGTCGGGCAGGGACGCCCAAGAGGCCCCGGGAGCATCGAG 982
                                                                                                                                                           ACCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAATAAC 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Grkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSU72251
Osyza sativa beta-1,3-glucanase precursor (Gns5) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Romero, G.O., Simmons, C., Yaneshita, M., Doan, M., Thomas, B.R. and Rodriguez, R.L. Characterization of rice endo-beta-glucanase genes (Gns2-Gns14) defines a new subgroup within the gene family Gene 223 (1-2), 311-320 (1998)
                                                                          AATTCCAATTTGATCAACCATGTGGGTCAGGGGAGGCCCGAAGAGGCCAGGGGCGATTGAG
                             863 GAGAGCGGGTCGTCGTCGGCGGCGCCGCCGACGCGCCGGCAACGCGCAAACGTAC
                                                                                                                                                                                                                                            TITGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTCACTTGAGAAATT
GAGAGTGGCTGGCCGTCAGCGGGCGGGACAGCGGCGACGTGTCTAATGCGCAGACTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .1834
/organism="Oryza sativa (japonica cultivar-group)
/mol type="genomic DNA"
/strain="M202"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="beta-1,3-glucanase precursor"
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/gene="Gn85"
920. .1831
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us-10-647-649-2.rge

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BD080855 3559 bp DNA linear PAT 27-AUG-2002 Banana proteins, DNA, and DNA regulatory elements associated with fruit development.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-1998 JP 2000512960
25-SRP-1997 US 60/060062
GREGORY MAY, STEPHANIE CLENDENNEN
C12N15/09, A01H5/00, COTX14/415, CO7X14/42, CO7X14/825, C12N5/10,
C12N9/08,
C12N9/10, C12N9/24, C12N15/00, C12N5/00
Banana proceins, DNA, and DNA regulatory elements associated
with fruit
                                                                                                                                                                                                                                                                          Musa acuminata
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Zingiberales, Musaceae;
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May,G. and Clendennen,S.
Banana proteins, DNA, and DNA regulatory elements associated with
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 TTTGCCATGTTCAACGAGGATCAGAAGCAGGCCGCAAGGGATTGAGAATAACTTTGGGCTG
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Patent: JP 2001517446-A 5 09-OCT-2001;
BOYCE THOMPSON INSTITUTE FOR PLANT RESEARCH INC
OS Musa acuminata (Danana)
PN JP 2001517446-A/5
                                                           973 TITIACCCTAACGAACAGCCTGTCTATTCGATCAGCTTC 1011
                                                                             Score 415.6; DB 6;
Pred. No. 4.6e-72;
0; Mismatches 294;
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Complement(1. .3559)
Location/Qualifiers
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/organism="Musa acuminata"
/mol_type="genomic DNA"
/db_xref="taxon:4641"
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BD080855.1 GI:22626458
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Best Local Similarity 68.2%;
Matches 670; Conservative 0
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                                                                                                                                                                                                  37.2%; Score 418.2; DB 15; Length 67.0%; Pred. No. 1.4e-72; ive 0; Mismatches 298; Indels
        /product=beta-1,3-glucanase=
<400. .469
/gene="Gns5"
/number=1
470. .908
/gene="Gns5"
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/gene="Gns5"
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/gene="Gns5"
/number=1
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Loadea; Triticeae; Hordeum.

1 (basea; Lo. 1249)
Troedason, U., Green, B., Widell, S., Collinge, D. and Bryngelsson, T.
Isolation and characterization of three beta-1,3 glucanases from fungus Blumeria graminis f. sp. hordei
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                                                                                           Length 1434;
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Pred. No. 8e-68;
0; Mismatches 328; Indels
 /evidence=experimental
1039. .1414
1415. .1434
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Best Local Similarity 64.9%;
Matches 617; Conservative
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TAMAKHGGSNVKLVYSSESGWFBSGGGTRAATPAARIYNQYLINHVGRGTPRHFGAIETY
VESMFNENQXDSGVEQUWGLFYPNMQHVYPISF"
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Triticum aestivum (bread wheat)

Triticum aestivum (bread wheat)

Triticum aestivum

Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticae, Triticum.

1 (bases III to 143)

Lai,D.M., Hoj,P.B. and Fincher,G.B.

Purification and characterization of (1-->3, 1-->4)-beta-glucan endohydrolases from germinated wheat (Triticum aestivum)
                                                                                 AGCGGGCGGACAGCGCGACGGTGTCTAATGCGCAGACTTACAATTTCAATTGATCAA
                                                                                                                             CCATGTGGGGTCAGGGGACGCCGAAGAGGCCAGGGGCGATTGAGACCTACATATTTGCCAT
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/function="cell wall metabolism"</pre>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Triticum aestivum"
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/db_xref="G1:840908"
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/EC_number="3.2.1.73"
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/chromosome="group 7"
/clone="lambda LW1"
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Fincher, G.B.
Direct Submission
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Search completed: April 7, 2006, 22:13:20 Job time : 6030 secs

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Adj11685 Rice DNA
Ada71217 Rice gene
Aeb66698 Rice geno
Aex33568 Rice gene
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Aci271558 Rice bere
Acx33554 Rice bere
Adx53559 Plant full
Aax33565 Rice Gns3

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Run on:

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Sequence:

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New nucleic acid sequence encoding beta-1,3-glucanase, useful for producing a transgenic plant with enhanced resistance against fungi.
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/*tag= a
/product= "Lily LPGlul protein"
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                                             AAX33568
ADA69783
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WPI; 2005-195288/20.
P-PSDB; ADY53161.
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Add 69575 Rice gene
Adz 69575 Rice gene
Adz 19801 Plant cDN
Adx 19801 Plant cDN
Aax 33567 Rice beta
Aax 3357 Rice beta
Aax 3557 Rice beta
Aax 3557 Rice beta
Aax 25612 Banana ri
Aax 25612 Banana ri
Aax 25612 Banana ri
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Aax 25612 Rice beta
Ady 220 (1-3,1-4)
Adx 5668 Plant ful
Adx 6661 Plant ful
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(without alignments)
10590.084 Million cell updates/sec
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                                                                                                                     Description
     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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The present invention relates to beta-1, 3 glucanase polynucleotide and its encoding polypeptide obtained from 111y plant. The invention is useful for producing a transgenic plant with enhanced resistance against a wide variety of stresses particularly fungal attack such as Botrytis blight and gray mold. The polypeptide of the invention is also capable of degrading the cell wall of fungi and thus can be used as an antifungal agent. The present sequence is 111y beta-1, 3 glucanase CDNA, IPGlul
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                                                                                                                                                                        1021 ATTTGATCAGATGAAATATAAATAAAAGGTCTTATATTGTAAGGCAAAGCTCGTAATTGA
TACAATTCCAATTTGATCAACCATGTGGGTCAGGGGACGCCGAAGAGGCCAGGGGGGGTT
                                                                           GAGACCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAAT
                                                                                                                                                AACTITIGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTCACTTGAGAA
                                                                                                                                                                                                                                                   1021 ATTTGATCAGATGAAATATAAATAAAGGTCTTATATTGTAAGGCAAAGCTCGTAATTGA
                                                 GAGACCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAAT
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Whitham S, Xie Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; SEQ ID NO 2898; 899pp; English.
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S, Tao
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illustrate the invention.
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Katagiri F, Quan S,
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(revised) (first en

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Clone C23; oil palm; regulatory sequence; beta glucanase activity;
tissue specific expression; mesocarp specific expression; fat; fatty oil;
                                                                                                                                                                                                                                                                                                                                      DNA sequence useful for isolating regulatory sequences for specific expression of proteins in monocots especially oil
                                                                  Clone C23; oil palm; regulatory
                                                                                      1,3 beta glucanase gene; ss.
                                                Mesocarp specific clone C23
                                                                                                        Elaeis guineensis; Jacq.
                                                                                                                                                                                                                                                            (UNIL ) UNILEVER NV.
(UNIL ) UNILEVER PLC.
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                                    GCAATCCCGAGAGGCGTGGAATCCATTGGGGTCTGCAATGGAATGGACGGTGACAACCTC
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tissue palm plant

activity"

protein" beta glucanase

Location/Qualifiers
28. .1047
/*tag= a
/product= "Clone C23 p:
/note= "Protein with b

99WO-EP004110

98EP-00305338

Stratford R;

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The patent discloses a method for isolating regulatory sequences using a beta glucanase gene. The regulatory sequence is used for tissue specific expression of endogenous and exogenous proteins obtained from monocot plants having drupaceous fruit. This promotes mesocarp specific expression thereby, increasing the amount of fat or altering the relative proportion of fatty acid in oil. Plants transformed with recombinant vectors comprising the regulatory sequence are used in food or pharmaceutical products. The present cDNA sequence is mesocarp specific clone C23 Gene specific probes derived from the C23 are used to isolate regulatory sequences from the mesocarp specific 1, 3 beta glucanase gene. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TCGGCAATCCCGAGAGGCGTGGAATCCATTGGGTCTGCAATGGAATGGACGGTGACAAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 430; DB 3; Length 1261
Pred. No. 1.1e-99;
0; Mismatches 350; Indels
Claim 2; Fig 3; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     38.2%;
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Matches 692; Conservative
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AAZ50051 standard; cDNA; 1261 BP

RESULT 3 AAZSO051 ID AAZ XX

534 564 654 684 744 774 834

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ATTGAGAATAACTTTGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTC 1011
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                                                                                                                                                                                                      385 GGAAATGAAGTGATTCCTGGAGCTGAAGCCCAATATGTGTGCTCCCTGCCATGAGAAACATC 444
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The invention relates a recombinant University of polymuclectide having any of 5544 nucleotide sequences (CDNAM SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 545-11088). The cDNAM and proteins are from corn, soyban, carbidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a producing a plant having an improved property, comprising transforming a production in a plant cell operably joined to a polymuclectide encoding a complexity is selected from improving plant cold tolerance, for manipulating growth rate in plant ells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for improving plant tolerance to extreme osmotic conditions, for improvement by modification of carbohydrate, mitrogen or phosphorus use and/or outer and for yield and/or content, for modification of carbohydrate, mitrogen or phosphorus use and/or under at least one stress condition. The polymucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biocemiles, in particular for producing transgenic plants with improved in the present invention are useful in the field of biocemiles, in particular for pathogens. They can also be used in physica
                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA constructs useful in the field of blochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.
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the printed specification, but was obtained in
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Pred. No. 5.9e-99;
0; Mismatches 323; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates a recombinant DNA construct comprising a
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segdata.uspto.gov/sequence.html?DocID=20040216190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 5127; 14pp; English.
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28-APR-2003; 2003US-00425115.
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Matches 656; Conservative
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seed protein yield.
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expression;

beta-glucanase; Gns; promoter; plant resistance; infection; transgenic monocotyledon; growth; ss.

98WO-US013525 97US-0050675P

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New polynucleotides which hybridise with rice beta-glucanase genes useful for transforming monocot plants for various characteristics including increased resistance to fungal infection.
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The present invention describes isolated polymucleotides (PN) comprising a sequence which hybridises under high stringency with a rice betaCC glucanase gene. Also described are: (A) a chimmeric gene (CGI) used to produce a transgenic monocot plant, comprising: (1) a transcriptional regulatory region which hybridises under high stringency with a rice beta equilatory region which hybridises under high stringency with a rice beta regulatory region, and (ii) a DNA sequence heterologous to the regulatory region, and encoding a protein to be produced by the plant; and (iii) a second DNA sequence encoding a signal polypeptide operatively linked 5 to 3', so that the signal polypeptide is in translation frame with the protein, and is effective to facilitate secretion of the protein across aleurone or scutellar epithelium layers into the endosperm of across aleurone or scutellar epithelium layers into the endosperm of across aleurone or scutellar epithelium layers into the endosperm of companient of monocot plant of method of enhancing the resistance of a monocot plant to fungal infection by stably transforming creasistance of a monocot plant with CGI, obtaining seeds from the cransforming a plant with CGI, obtaining seeds from the cransforming a plant with CGI, obtaining the characteristics of a rice beta-glucanase enzyme, corresponding to beta-glucanases 2-9 (Gns 2-9). The polymucleotides of the invention are useful to transform monocot correspondence to fungal infection, improved growth characteristics, and high expression levels of heterologous proteins in companience con funcased resistance to fungal infection, improved growth 183 GCAATCCCGAGAGGCGTGGAATCCATTGGGGTCTGCAATGGAATGGACGGGGAAACCTC 123 63 57 TACAGCCCCGACCAGAGCCATCCAGGCCTCTAACATCTACCTCATCCTC 1 ATGGCAAAGCATGGCGTTGCTTCCGTTTTAACACTGGCATTGGTCCTTGGAG---TTGCG 4 ATGCCAGCTCAGCACATCATCTCCATGGCTGCCATCCCTCCTTGTAGTACTCTCG Gaps 37.9%; Score 426.4; DB 2; Length 993; 66.2%; Pred. No. 8.3e-99; tive 0; Mismatches 326; Indels 15; Sequence 993 BP; 189 A; 345 C; 297 G; 162 T; 0 U; 0 Other; Disclosure, Page 67-68; 90pp; English. Query Match
Best Local Similarity 66.2
Matches 667; Conservative 118 g 셤 8 ઠે ò

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AAX33567 standard; DNA; 993

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(first entry)

07-JUL-1999

AAX33567;

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98WO-US013525 97US-0050675P

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Rodriguez RL

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Rice; beta-glucanase; Gns; promoter; plant resistance; expression; fungal infection; transgenic monocotyledon; growth; ss. Rice beta-glucanase gene Gns5. WO9859046-A1. 07-JUL-1999 30-DEC-1998 fundal Oryza

The present invention describes isolated polymucleotides (FV) comprising a sequence which hybridises under high stringency with a rice betaglucanase gene. Also described are: (A) a chimeric gene (CG1) used to glucanase gene. Also described are: (A) a chimeric gene (CG1) used to groduce a transgenic monocot plant, comprising; (1) a transcriptional regulatory region which hybridises under high stringency with a rice beta glucanase promoter; and (ii) a DNA sequence heterologous to the regulatory region, and encoding a protein to be produced by the plant; and (iii) a second DNA sequence encoding a signal polypeptide operatively linked 5' to 3', so that the signal polypeptide is in translation frame with the protein, and is effective to facilitate secretion of the protein across aleurone or scutellar epithelium layers into the endosperm of seeds obtained from the plant; (B) a monocot plant stably transformed cross stance of a monocot plant to fungal infection by stably transforming the resistance of a monocot plant to fungal infection by stably transforming a plant with CG1, obtaining seeds from the entangence of the seeds and obtaining the protein from the seed endosperm; (F) an isolated protein having the characteristics of the polymucleotides of the invention are useful to transform encoct plants. The polymucleotides and the proteins produced may also provide the arrear arrearies in the increased resistance to fungal infection, improved growth comprising characteristics, and high expression levels of heterologous proteins in New polynucleotides which hybridise with rice beta-glucanase genes useful for transforming monocot plants for various characteristics including increased resistance to fungal infection. present invention describes isolated polynucleotides (PN) various tissues obtained from the plant Claim 1; Page 30; 90pp; English. WPI; 1999-105620/09.

Sequence 1834 BP; 446 A; 507 C; 460 G; 421 T; 0 U; 0 Other; Indels Score 418.2; DB 2; Pred. No. 1.3e-96; Mismatches 298; ; 0 17.2%; al Similarity 67.0%; 629; Conservative (Best Local Similarity Query Match Matches

1024 192 964 133 GCCGACGTCGTCAACCTCTACAAGTCCAACAACATAGCTGGCATGCGACTCTACAGCCCC 965 AGCGACGTGCAGCTCTACAAGTCCAACGGCATCGACTCCATGACTCCATCTACCA AGAGGCGTGGAATCCATTGGGGTCTGCAATGGAATGGACGGTGACAACCTCCCCCAGCCC 193 GACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAACATCTACCTCATCCTCGACGTCCCC 905 73 g g ઠે 8 ò

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433 TCTGCCGGCCTTCAGAACATCAAGGTCTCCACATCAGTCTCCTTCGGCGTCGTCGGTACC 492

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                                  493 TCATATCCCCCCTCAGCTGGCTCCTTCTCTTCCGATGCATCGTCGACATTGGGTCCAATC
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P-PSDB; AAY05889, AAY05840, AAY05841.
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             This is the nucleotide sequence of a DNA molecule termed GLUC. The invention provides isolated DNA molecules which are differentially expressed during banana fruit development, and the protein products of these genes. The DNA is selected from a group comprising starch synthase, chitinase, endochitinase, beta-1,3-glucanase, thaumatin-like protein, protein. The regulatory elements of the genes can be used to produce chimeric genes for transformation of plants to provide controlled expression of heterologous DNA during fruit development, or in response to exogenous developmental signals, such as ethylene signals. The heterologous protein, e.g. a therapeutic protein, can be isolated from the fruit or consumed directly in the transformed fruit. The identity of the present sequence is not given. The entire DNA sequence has been decoded in all 3 reading frames to provide the amino acid sequences given
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Pred. No. 7.7e-96;
0; Mismatches 294;
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West Local Similarity 68.2%;
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GAGCGGGTGGCCGTCGGCGGGCGGAGGCGAAGCGAGCACCAGCAACGCGCAGACGTA 2857
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                            CAATTCCAATTTGATCAACCATGTGGGTCAGGGGACGCCGAAGAGGCCCAGG---GGCGAT
                                                    TGAGACCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                       expression;
                                                                                                                                                                                                                                                                                                                                                                                                                    Rice; beta-glucanase; Gns; promoter; plant resistance; fungal infection; transgenic monocotyledon; growth; ss.
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a rice beta-glucanase enzyme, corresponding to beta-glucanases 2-9 (Gns 2-9). The polymuclectides of the invention are useful to transform monocot plants. The polymuclectides and the proteins produced may also provide increased resistance to fungal infection, improved growth characteristics, and high expression levels of heterologous proteins in various tissues obtained from the plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes the 1463bp cDNA of barley (1-3,1-4)-beta-glucanase isoenzyme EI. This sequence is derived from a transcript from the distal promoter of the (1-3,1-4)-beta-glucanase isoenzyme EI gene. (See also AAQ24290.) EI is synthesized in germinating barley grain where it acts to depolymerise the beta-glucans in the cell walls of the starchy endosperm. Low levels of the enzyme leads to high levels of the glucans and this can cause a reduced malt quality, serious filtration difficulties in the product. The isolated EI gene can be transfered to plants to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product. The isolated EI gene can be transfered to plants to generate varieties which have improved malting and brewing properties. Alternatively the gene can be introduced into yeast to remove residual beta-glucan in beer prodn. This protein can be mutated to generate a m
                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding barley (1-3,1-4)-beta-glucanase isoenzyme(s) E1 and E1:
1 to improve quality of barley for malting and brewing processes
                                                                                                                                            88
                                                                                                                                         promoter; EI; beta-glucan; endosperm; beer production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1463 BP; 303 A; 468 C; 421 G; 271 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 408.6; DB 2;
Pred. No. 3.5e-94;
0; Mismatches 359;
                                                                                                                         EI (2).
CAGCCTGTCTATTCGATCAGCTTC 1011
           889 TCGCCGGCATACTCCATCAATTTC 912
                                                                                                                                                                                Location/Qualifiers
                                                                                                                       (1-3,1-4)-beta-glucanase isoenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 9; 75pp; English
                                                               AAQ24291 standard; DNA; 1463 BP
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                                                                                                                                                                                           68. .1072
                                                                                                                                                                                                                                                                                                                                                                  (UYLT-) LA TROBE UNIV.
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Tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR23602
                                                                                                                                                            Hordeum vulgare.
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ATGGCAGGCCAAGGCGTTGCCTCCATGTTGGCTCTGGCATTGCTCCTCGGAGCCTTCGCC 127

ATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTTGTAGTACTCTCG

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drought tolerance; disease resistance; growth rate; drought tolerance; disease resistance; galactomannan production; disease resistance; merbicide tolerance; lighin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed protein yield.
                                                                                           18-DEC-2003; 2003US-00739930.
                                                                                                       2003US-00424599
                                                                                                            28-APR-2003; 2003US-00425115
      Plant cDNA, Seg ID 5007
                                                                                                                                               WPI; 2004-757369/74.
                                                                                                                        (KOVA/) KOVALIC D K.
                                                                   US2004216190-A1
                                                        Viridiplantae.
                                                                                                      28-APR-2003;
                                                                               28-OCT-2004
                                                                                                                                   Kovalic DK
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New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.

Claim 1; SEQ ID NO 5007; 14pp; English.

The Invention relates a recombinant DNA construct comprising a polymerleotide having any of 5544 nucleotide sequences (CDNAB SEG ID NO: 1-5549) and encoding a polypeptide with any of 5544 amino acid sequences (1-5549) and encoding a polypeptide with any of 5544 amino acid sequences (1-5549) and encoding a polypeptide with any of 5544 amino acid sequences (1-5549) and encoding a polypeptide and procession of the comprising transforming a gequence is detrived from which organism. Also included is a method of producing a plant call operably joined to a polymucleotide encoding a plant with a recombinant DNA construct comprising a promoter region to plant with a recombinant DNA construct comprising a promoter region of plant with a recombinant DNA construct comprising a promoter region of plant with a recombinant DNA construct of plant with a recombination in plant cells by modification of the cell cycle plant. The property is selected from improving plant colerance to plant disease, for glactomannan production, for production of pathway, for improving plant disease, for improving plant tolerance to plant disease, for improving plant tolerance to perhodus recombination in plants, for improving plant tolerance to extreme osmocit conditions, for improving plant tolerance to extreme osmocit conditions, for improving plant tolerance to pathogens or peats, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and each or actor. The methods and compositions of the present under at least one stress condition. The polymucleotide may also encode a plant transcription for providing improved plants with improved biological characteristics such as increased yield, improved in particular for producing transgenic plants with improved colerance to extreme osmocit and drought conditions, and improving plant colerance to plant peatent sequence is of the invention are useful in the field of biochemistry and colerance to plant peater invention relates a recombinant DNA construct comprising a electronic format directly from USPTO at segdata.uspto.gov/seguence.html?DocID=20040216190.

Sequence 1458 BP; 310 A; 436 C; 417 G; 295 T; 0 U; 0 Other;

AAQ24292 standard; DNA; 1257 BP.

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Score 394.2; DB 13;
Pred. No. 1.7e-90;
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 35.0%;
64.9%;
Query Match
Best Local Similarity 64.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGCBCCGAGCACCGTCGTGAGCATGTTCAAGTCCAACGGGATCAAATCGATGGTGCGCTG 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomanan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polymucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ffp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAACGCGCTGAACGCGCTGAGCGGCACCAGCATCGGGCTCATCATGAACGTGCCCAACAC
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Cao
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Pred. No. 2.7e-87;
0; Mismatches 359; Indels
                                                                                                                                                                                                                                                                                                                                        Tabaska JE,
                                                                                                                                                                                                                                                                                                                                        Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 26408; 15pp; English.
                                                                                                                         28-APR-2003; 2003US-00425114.
                                                                                                                                                           06-MAY-1999; 99US-00304517, 05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                        Kovalic DK,
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al Similarity 62.9%;
629; Conservative
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(SCRE/)
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          sig_peptide
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                                                                              WO9205258-A
                                                                                   02-APR-1992
                         misc_signal
                                   TATA_signal
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This sequence 'Encodes (1-3,1-4)-beta-glucanase isoenzyme EI gene, showing the two promoter regions, the distal and proximal promoters. The two transcripts produce the same mature protein but have different signal peptides. The transcript from the distal promoter is 4169pp long and contains an intron of 2513bp. This intron is unusually long for a plant intron which have an average length being 249bp. The signal peptide produced from this transcript is 28 amino acids long. The transcript from the distal promoter is 3807bp and contains an intron of 54bp. The signal peptide produced from this transcript is 23 amino acids long. There is some evidence that suggests that these differing introns may have some roole in exon "shuffiling". BI is synthesized in germinating barley grain where it acts to depolymerise the beta-glucans in the cell walls of the starch where it acts to depolymerise the beta-glucans in the cell walls of the starch where it acts an cause a reduced malt quality, serious filtration difficulties in the brewing process and can contribute to haze formation to the final product. The isolated BI gene can be transfered to plants to generate varieties which have improved malting and brewing properties.

Alternatively the gene can be introduced into yeast to remove residual the pharmals and this an experience of the product in the brewing protect of the subject of pervises.

Alternatively the gene can be introduced into yeast to remove residual the pharmals and the product. This protein can be mutated to generate a more the product.
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1 to improve quality of barley for malting and brewing processes.
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   Score 380.8; DB 2;
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33.8%;
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ADL18243 standard; DNA; 4849 BP

ADL18243 ID ADL1 XX

Sequence 4643 BP; 1166 A; 1190 C; 1110 G; 1177 T; 0 U; 0 Other;

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27-MAR-2002; 2002US-0368327P.
04-APR-2002; 2002US-0370620P.
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KATAGIRI F.
KREPS J.
MOUGHAMER T.
PROVARI N.
RICKE D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid markers on wheat genetic background. The primer set is useful for detecting nucleic acid markers derived from barley chromosome on wheat genetic background. The primer set is useful for determining whether the long arm of 1H chromosome of barley has been introduced into wheat, and for determining fertility of wheat. The method enables detection of nucleic acid markers derived from long arm of 1H chromosome of barley on wheat genetic background. The present sequence represents a barley gene used to design PCR primers ADL18230 and ADL18231 of the
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                                                                                                                                                                                                                                                                                                 barley; wheat; chromosome 1H; fertility; gene; ds.
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Pred. No. 7.1e-87;
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Best Local Similarity
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polymucleotides that are modulated by post-transcriptional gene silencing polymucleotides that are modulated by post-transcriptional gene silencing (FYGS). Specifically, it refers to the regulation of gene expression in plants via PTGS and the trans-activation of homologous genes due to increased RNA degradation. The present invention describes clusters of polymucleotides from cereals, in particular rice, as well as homologues and the polypeptide sequences derived thereof, where gene expression is altered in response to PYGS. As such, the elucidation of gene silencing mechanisms can lead to more efficiently expressed transgenes, and can also improve the understanding of plant-viral interactions and targeting the suppression of specific plant genes. This polymucleotide sequence is a rice CDNA sequence where expression is modulated by gene silencing. Contappers in the printed specification but has been obtained in electronic format from the US patent office at electronic format from the US patent office at the sequence contapped to the contapped useful for modulating gene expression within a cell ä This invention relates to a novel method for identifying isolated s SP, Cooper B, Glazebrook J; Moughamer T, Provart N, Ricke Example 15; SEQ ID NO 439; 79pp; English H, Briggs SP, Kreps J, Mough posttranscriptional gene silencing. Chang Wang X, Chang Katagiri P, 2003-829655/77 New polynucleotide, WPI; 2003-829655 P-PSDB; ADJ11804 Goff SA, ል \$XCCCCCCCCCCX\$X\$4\$X\$4\$X\$4\$

Sequence 1110 BP; 197 A; 326 C; 402 G; 185 T; 0 U; 0 Other;

Gaps / Match . 31.5%; Score 354.2; DB 11; Length 1110; Local Similarity 60.9%; Pred. No. 2.7e-80; hes 613; Cobservative 0; Mismatches 388; Indels 6; Query Match Best Local Si Matches 613

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850 243 303 363 423 613 553 543 603 1029 ATGGCTAGCCAAGGTGTAGCCTCCATGTTCGCTCTCGCATTGCTCCTCGGTGCCTTTGCC 970 910 790 730 670 483 GCAATCCCGAGAGGCGTGGAATCCATTGGGTCTGCAATGGAATGGACGGTGACAACCTC 123 CCCCAGCCCGCCGACGTCGACACCTCTACAAGTCCAACATAGCTGGCATGCGACTC 183 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCCTTGTAGTACTCTCG 63 969 TCCATTCCTCAAAAGGCGGAGGCGATGTGCTACGGCTACGGCATGAGCGTG 909 CCGCCGCGAGCTCGGTGGGGATGTACCGCTCCAACGGCATCACGTCGATGGGGCTG TACAGCCCCGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAACATCTACCTC 849 TACGCGCCGCACCAGGCGCCCCCAGTCGGTGGGCGCACGGGGATCAGCGTCGTCTC GACGTCCCCAACTCCGACCTCCAAAACATTGCCTCCGACCAATCCGCCGCCGCCAACTGG GGGGGGCCAACGACGTCTCCAACCTCGCCGCCAGCCCGCCGCCGCGCGCTCGTGG GTCCAAACCAACGTCCAAGCCTACCCAAACGTTGCCTTCCGATACATCGCCGTCGGAAAC GAAGTCATCCCCGGCGGCCAAGCTCAGTACGTCCTCCCAGCCATGAACAACATACAGTCC dade - - redecedececeacerecaecraecraeceareacaaaaacareeceec GCCCTCTCCTCTGCCGGCCTTCAGAACATCAAGGTCTCCACATCAGTCTCCTTCGGCGTC decretegreresecreseccaeareaseses de la conservación de la consecuencia del la consecuencia del la consecuenc GTCGGTACCTCATATCCCCCCTCAGCTGGCTCCTTCTCTTCCGATGCATCGTCGACATTG 64 124 184 244 789 304 729 364 699 424 612 484 552 544

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DR731420 FCASC01041
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CC646871 OGUISBUTH
CB670194 OSUNEC03C
BF265541 HV CB2011
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CB657742 OSUNEC12U
CR651742 OSUNEC12U
CL656551 OSUNEC13U
CR655744 OSUNEC04G

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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Oryza sativa (indica cultivar-group)

EWaryorta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Ewaryorta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaee; Oryzae; Oryzaee; Oryzaee
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/organism="Oryza sativa (indica cultivar-group)"
/mol_typeagenomic DNA"
/db xref="taxon:39946"
/clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
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Email: chenchen@genomics.org.cn
AJ613783
CL9660877
CY66157
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Location/Qualifiers
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GSS.
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Triticum aestivum (bread wheat)
Triticum aestivum (bread wheat)
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

El (bases 1 tro 1109)
S Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Linke, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L., Monroy, A., Muzak, I., Nilson, D., Pentional Genomics of Abiotic Stress In Wheat and Canola Crops Contact: Patrick Gulick
Plant Molecular Biology

(default parameters) has been run on this sequence. Lucy identified the region [37,809].

Plate: STG1 row: F column: 10.

1. .1109

/organism="Triticum aestivum"

source

Email: pgulick@alcor.concordia.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software lucy

Canada

Concordia University, Department of Biology 7141 Sherbrooke St. West, Montreal, Quebec H4B 1R6, Tel: 514 848 2824 Ext 3407 Pax: 514 848 2881

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KEYWORDS
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/mol_type="mRNA"
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/db xref="taxon:4565"
/clone lib="riticum and leaf; Vector: pCMV.SPORT6; Aerial
/clone lib="riticum and leaf; Vector: pCMV.SPORT6; Aerial
parts (crown and leaf) of wheat cultivar Norstar from
control and long exposure times to low temperature. 4 mRNA
populations were combined before constructing the library;
7 days non-acclimated plants and 1, 23, and 53 days
cold-acclimated at 4C. Non-acclimated and cold-acclimated
plants were grown in vermiculite This is the only library
that was done according to the Invitrogen manual, and
therefore, a percentage of clones will not have the 3
prime end because of Not1 digestion within the cDNA."
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Best Local Similarity 63.1%;
Matches 645; Conservative
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SCJLRT1023E06.g Saccharum officinarum mRNA (Nogueira,F.T.S)
Saccharum officinarum cDNA, mRNA sequence.
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Spermatbphyta, Magonlophyta; Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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Arruda, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAATAACTTTGG
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C.P. 6176, Campinas, SP 13083-970, Brazil
Tel: 55 19 37881101
Fax: 55 19 37881089
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/mol_type="mRNA"
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Location/Qualifiers
1. .1307
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Bioinformatics Lab
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FGAS022241 Triticum aestivum FGAS: Library 5 GATE 7 Triticum aestivum CK210431. GI:39572821 ESEC-2003 CK210431. GI:39572821
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Triticum aestivum
Triticum aestivum
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
I (bases I to 1107)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., and Sarhan, F.
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eprhartoideae; Oryzae; Liliopsida; Poales; Poaceae;

Enthartoideae; Oryzae; Liliopsida; Poales; Poaceae;

Enthartoideae; Oryzae; Liliopsida; Poales; Poaceae;

Ba,L., Wango,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,

Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,

Mong,G.K.S., Deng,X.W. and Wang,J. Sun,D., Zhao,H., Yuan,L.,

Mong,G.K.S., Deng,X.W. and Wang,J.

An analysis of transcriptional regulation of the rice genome and

its comparison to Arabidopsis

Unpublished (2004)

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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="genomic By46"
/clone llb="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
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/Mol type="nRNA"
// (Ab) type="nriticum aestivum FGAS: Library 5 GATE 7"
// (Ab) type="nriticum aestivum FGAS: Library 5 GATE 7"
// (Ab) type="nriticum"
// (Ab) type= This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [18,757].

Plate: L58022 row: N column: 22. 2 183 408 363 468 525 243 303 483 109 Ardácica acciración de contración de la productiva de la Ardación de la Ardac GCAATCCCGAGAGGCGTGGAATCCATTGGGGTCTGCAATGGAATGGACGGTGACAACCTC 123 169 TCCATCCACAAAGCGTCGAGTCCATCGGAGTGTGTGCTACGGCATGAGCGCCCAACAACAACTG 229 cogcogocacocorocitorcacaroritorascicoracocaroracocorocitos 288 289 TACGCCCCCGACACAGGCGCGCTGCAGGCCGTCGGCGCGCCACGGCGTCAACGTCGTCGTCGTC 348 GAAGTCATCCCCGGCCCAAGCTCAGTACGTCCTCCCAGCCATGAACAACATACAGTCC 423 GICGGTACCICATATCCCCCCTCAGCTGCTCCTTCCCATGCATCGTCGACATTG 543 705 ATGGCÅGCTCAGCACATGCCTGCCATGCCATGCCATCCCTTGTAGTACTCTCG GGTCCAATCATACAGTTTCTAGCCAGCAATGGCTCCCCATTACTTGCCAACATCTACCCC CCCCAGCCCGCCGACGTCGTCAACTCTACAAGTCCAACAACATAGCTGCGACTC TACAGCCCCGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAACATCTACCTCCATCCTC GACGTCCCCAACTCCGACCTCCAAAACATTGCCTCCGACCAATCCGCCGCCACCAACTGG GTCCAAACCAACGTCCAAGCCTACCCAAACGTTGCCTTCCGATACATCGCCGTCGGAAAC GCCCTCTCCTCTGCCGGCCTTCAGAACATCAAGGTCTCCACATCAGTCTCCTTCGGCGTC cricidedergranacaccicciccricedericerricaceggadeseggacecerrearie Gaps 4, 30.5%; Score 343; DB 7; Length 1107; 63.3%; Pred. No. 6e-82; tive 0; Mismatches 319; Indele 1. .1107 /organism="Triticum aestivum" 556; Conservative Similarity Query Match Best Local Si Matches 556, 484 64 124 184 244 304 409 364 469 424 526 586 544 646 FEATURES 셤 ઠે 셤 ò 셤 ð 셤 δ 요 ð 셤 ઠે g ઠે g ઠે g ઠ

Triticum aestivum (bread wheat)

Triticum aestivum

Triticum aestivum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticae; Triticum.

E 1 (bases 1 to 1025)

S Allard, F., Crosby, W.L., Danyluk, J., Rudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D.,
Penniket, C., Roach, J.L. and Sarhan, P.
Punctional Genomics of Abiotic Stress In Wheat and Canola Crops
L. Unpublished (2003)

Contact: Wm L Crosby

Bioinformatics Figure 1: fgae estagos.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [27,866].
Plate: Location/Qualifiers CK162463 1025 bp mRNA linear EST 05-DEC-2003 FGAS015057 Triticum aestivum FGAS: Library 4 Gate 8 Triticum aestivum cDNA, mRNA sequence. 783 885 843 945 663 706 TACCTGGCCTGGGCCTACAACCCGAGCGCCATGGACATGAGCTACGCGCTCTTCANCGCG TCTGGTACAGTCGTACAGGACGGGTCCTACGCTTACAACAACCTCTTCGATGCCATGGTC GACGCATTGTACTCGGCCCTGGAGAGCGCCGAAGGGCCGAATGTCCCTGTTGTCGTGTCG GACGCCTTCTACACGCCCATGCCCAAGCACGCGCCTCCAACGTGAAGCTGGTGGTGCTCC GAGAGTGGCTGGCCGTCAGCGGGGGCGGCGGCGGTGTCTAATGCGCAGACTTAC 886 GANAGCGGGTGGCCGCGGGGGGGGCCACGGCGACCCCCGGCGAACGCCAGGATCTAC TACTTGAGCTATGCTGGCAACTCCGGATCCATCGACCTCTCATACGCCCTCTTTACTGCA University of Saskatchewan, Department of Computer Scier 1C101 Engineering Building, 57 Campus Drive, Saskatcon, Saskatchewan, S7N SA9, Canada Tel: 306 966 1769 844 AATTCCAATTTGATCAACCATGTGGGTCAGGGGACGCCG 882 /organism="Triticum aestivum" CK162463.1 GI:38991695 604 664 991 724 826 784 946 source DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT REFERENCE AUTHORS RESULT 6 CK162463 FEATURES 셤 δ 셤 ઠે g ò 요 ò 셤

Best_Loca Matches

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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
I (bases 1 to 1014)
Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
Manalysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
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/mol type="genomic DNA"
/mol type="genomic DNA"
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/note="Oryza sativa exon trapped genomic
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Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300,
Th: 86-10-80481559
Pax: 86-10-80488676
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llarity 61.0%; Pred. No. 9.7e-82;
Conservative 0; Mismatches 368;
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Rice genomic sequence.
Class: exon-trapped.
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ACCESSION VERSION KEYWORDS

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growth chamber for 7 days under an irradiance of 200 mmol m-2 sec-1. The temperature was maintained at 20 degrees C with a 15-hr photoperiod under a relative humidity of 70%. After this period watering of plants was stopped. Four time points were sampled during a two week period; the first after wilting was observed and the last, two weeks later, consisted of live crown and leaf tissue (leaf tissue that was yellow was not included in sampled material). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with Not!."
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Pred. No. 8.4e-81;
0; Mismatches 305;
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Best Local Similarity 63.4%;
Matches 533; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                943 CCGCAAGGGATTGAGAATAACTTTGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCG 1002
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                                                                                                                                                                                        762
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                                                                                                                                                                                                                                                                                                                                                                 820 ACCGACATCGCGCGGACCTACGTGCAGAACCTCGATTAAGCATGCGAAGAAGAGGGCGCG
                                                                                                     TACGCCACGTTCCAGGCCGCCACGAGGCCCGACCCCAACACCGGCCTGGTCTACACC
                                                                                                                                                                                                                                                                                                                       GTGTCTAATGCGCAGACTTACAATTTCCAATTTGATCAACCATGTGGGGGACGCCG
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This sequence is the direct result of the Bas
Phred (default parameters). It is the raw bas
identification of the high quality insert the
(default parameters) has been run on this seq
the region [34,806].
Plate: L4B001 row: B column: 04.
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                                 TACGCCCTCTTTACTGCATCTGGTACAGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum (bread wheat)
Triticum aestivum
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/db_xref="taxon:4565"
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COMMENT

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671 663 723 791 783 851 843

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950 bp DNA linear GSS 26-AUG-2003
Zea mays genomic clone ZMMBMa0726A22,
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 950)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic_DNA library"
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/strain="B73"
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↓./organism="Zea mays"

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Class: methylation filtered
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Email: whitelaw@tigr.org
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genomic survey sequence.
CG352135
CG352135.1 GI:34269401
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OBIFCC004630 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryza, Oryza,
1 (baes 1 to 1022)
Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Mang,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., An analysis of transcriptional regulation of the rice genome and unpublished (2004)
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                                                                                                                           Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
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Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
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Department of Bioinformatic
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/organism="Oryza sativa (indica cultivar-group)"

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CL982353 1020 bp DNA linear GSS 21-SEP-2004
OBIFSCO47411 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
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Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bhrhartoideae; Oryzae, Oryza.

I (bases 1 to 1020)
Ma.L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
Man analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
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/clone_lib="Oryza sativa Express Library"
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Best Local Similarity 61.9%;
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OBIFCCO04627 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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CL960504.1 GI:52375712
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Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Birhartoideae; Oryzaes; Oryza.
1 (bases 1 to 1005)
Ma.L., Wangc.J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y.,M.Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., An analyais of transcriptional regulation of the rice genome and its comparison to Arabidopsis
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/mol_type="genomic DNA"
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Bejjing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300,
Tel: 86-10-80481559
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Email: chenchen@genomics.org.cn
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Oryza sativa (indica cultivar-group)

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Bukaryotta; (indica cultivar-group)

Bukaryotta; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

Brhartoideae; Oryzeae; Oryza.

I (bases 1 to 1005)

Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Macng,G.K.S., Deng,X.W. and Wang,J.

An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

AL Unpublished (2004)

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/mol_type="genomic DNA"
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Rice genomic sequence.
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Spermarophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
Clade; Panicoidaea; Andropogoneae; Zea.
1 (bases 1 to 927)
Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Consortium for Maize Genomics
Unpublished (2002)
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/clone="zxMBMa0851A05"
/clone lib="zxM 0.7 l.5 KB"
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9712 Medical Center Drive, Rockville, MD 20850, USA
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0; Mismatches 339; Indels
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/strain="B73"
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers
1. .927
/organism="Zea mays"
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                                                                                                                     Gaps
            /clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
                                                                                                                    15;
                                                                                  1005;
                                                                                    Length
                                                                               Score 320.4; DB 10; Length
Pred. No. 8.4e-76;
0; Mismatches 381; Indels
xref="taxon:39946"
                                                                                28.5%;
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                                                                                Query Match
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CL959613
OBIFCC003223 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae; Oryza.

1 (bases 1 to 1017)
Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Yiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and unpublished (2004)
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Department of Bioinformatic
Bejijang Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
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/organism="Oryza sativa (indica cultivar-c/organism="Oryza sativa (indica cultivar-c/mol_type="genomic DNA"
/mol_type="genomic DNA"
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                       AACAAGTCGCCCGTGTATCCCATCCGGTTC
  AACGAACAGCCTGTCTATTCGATCAGCTTC
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Rice genomic sequence.
Class: exon-trapped.
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                                                                              CCAGCAATGGCTCCCCATTACTTGCCAACATCTACCCCTACTTGAGCTATGCTGGCAACT 625
                                                                                              626 CCG------GATCCATCGACCTCTCATACGCCCTCTTTACTGCATCTGGTACAG 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.2%; Score 418.2; DB 3; llarity 67.0%; Pred. No. 4.6e-110; Conservative 0; Mismatches 298;

    Sequence 4, Application US/09105390
    Patent No. 6288303
    GENERAL INFORMATION:
    APPLICANT: Rodriguez, Raymond
    TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
    TITLE OF INVENTION: and Genes

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: US/09/105,390 FILING DATE: Filed herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REPEREBRICK JOCKET NUMBER: 2000-0455.30
TELECOMINICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-UNW-97
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 1834 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
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US-09-105-390-4
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nes 629; Conserv
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                                      US-09-105-390-4
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Score 426.4; DB 3; Length
Pred. No. 1.4e-112;
0; Mismatches 326; Indels
   37.9%;
                                                                    Matches 667; Conservative
                                      Similarity
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                                                                                                                                                                                                                                                                                                     Score 411.2; DB 3;
Pred. No. 3.3e-108;
0; Mismatches 293;
     FELECOMMUNICATION INFORMATION
                                                                               39
                                                                                                                                                                                                        NAME/KEY: Coding Sequence LOCATION: 1...912
COTHER INFORMATION:
US-09-105-390-39
                                                                                                                                                                                                                                                                                                     36.6%;
                                                                     INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 912 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 67.0°
Matches 619; Conservative
                       TELEPHONE: 650-324-080
TELEFAX: 650-324-0960
TELEX:
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                                                                                                    1322 GGCTTCCCGCCGCCCCGCGCGCTCTCCGCC----TCGGACATGGGCCCCATA 1372
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TCTGCCGGCCTTCAGAACATCAGGTCTCCACATCAGTCTCCTTCGGCGTCGTCGGTACC
                     493 TCATATCCCCCCCCCCGGCTCCCTTCTCCGATGCATCGTCGACATTGGGTCCAATC
                                                                                                                                                                                                                                                                                                 GTCGTACAGGACGGGTCCTACGCTTACAACAACCTCTTCGATGCCATGGTCGACGCATTG
                                                                                                                                            553 ATACAGTITCTAGCCAGCAATGCCTCCCATTACTTGCCAACATCTACCCCTACTTGAGC
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TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATYONEY/ABENT INFORMATION:
NAME: PETILION VUMBER: P42,995
REGISTRATION NUMBER: P42,995
REFERENCE/DOÈWET NUMBER: 2000-0455,30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/09105390 Patent No. 6288303
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30.8%;
                                                                                                                                                                             Query Match
Best Local Similarity 60.4*
Matches 611, Conservative
    polyA_signal
                                                                                         NAME/KEY: mat_peptide
; LOCATION: 133.1050
US-08-457-797A-11
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                                                                   GAGGATCAGAAGCAGCCGCAAGGGATTGAGAATAACTTTGGGCTGTTTTACCCTAACGAA 987
not shown."
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/function= "glucanase"
/product= "preprotein of the glucanase GluG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEX: 3'UTR
LOCATION: 1051..1235
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "14 nucleotides at the 3'end not s
FRATURE:
NAME/KEY: polyA_signal
LOCATION: 1083..1088
OTHER INFORMATION: /note= "potential polyadenylation signal"
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIREL.

CIITY: New York

CITY: New York

COUNTRY: U.S.A.

ZIP: 1011-2012

ZIP: 1011-2012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: TBM FC compatible

COMPUTER: TBM FC com
                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic pathogen-resistant organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                             988 CAGCCTGTCTATTCGATCAGCTTC 1011
                                                                                                                                                                                                    rceccescaraciccarcarric 912
                                                                                                                                                                                                                                                                        RESULT 4
US-08-457-797A-11
Sequence 11, Application US/08457797A
Patent No. 5689045
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 1235 base pairs TYPE: nucleic acid STRANDEDNESS: single
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Hordeum vulgare
STRAIN: L.
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NAME/KEY: CDS
LOCATION: 49.1050
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Tx
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
LOCATION: 1210.71215
OTHER INFORMATION: /note= "potential polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                        Length 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Score 346.2; DB 2;
Pred. No. 2.1e-89;
0; Mismatches 388;
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64 GCAATCCCGAGAGGCGTGGAATCCATTGGGTCTGCAATGGAATGGACGGTGACAACCTC 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.8%; Score 346.2; DB 2; Length 60.4%; Pred. No. 2.1e-89; ive 0; Mismatches 388; Indels
                                                                                   OTHER INFORMATION: /note= "potential polyadenylation OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 60.4 Matches 611; Conservative
                                       1210..1215
                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-812-025-11
                                       COCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304
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940 GAGACGTACATCTTCGCCATGTTCAACGAGAACAGAAGACCGGGGACGCCACGAAGAGG 999
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NAME/KEY: CDS
LOCATION: 49..1050
OTHER INFORMATION: /partial
OTHER INFORMATION: /codon gtart= 49
OTHER INFORMATION: /function= "glucanase"
OTHER INFORMATION: /product= "preprotein of the glucanase GluG"
OTHER INFORMATION: /product= "preprotein of the glucanase GluG"
OTHER INFORMATION: /partial
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "14 nucleotides at the 3'end not shown."
                                                                                                                                                                       961 AACTITIGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTC 1011
                                                                                                                                                                                                                                                                            1000 Agciricegecrirca accesaca a grande de la seconta ca de la company d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic pathogen-resistant organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUTTY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,025
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Tenser, Arthur
REGISTRATION NUMBER: 18,839
NAME: Kole, Lisa
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
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LOCATION: 1083..1088
OTHER INFORMATION: /note= "potential polyadenylation
OTHER INFORMATION: signal"
FEATURE:
NAME/KEY: polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Transgenic pathogen-resistant on NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond STREET: 30 Rockefeller Plaza
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08812025
Patent No. 5804184
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 238555
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 1235 base pairs TYPE: nucleic acid
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
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LOCATION: 11.48
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Length 1235;

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NAME/KEY: mat_peptide LOCATION: 133..1050
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LOCATION:
US-09-138-873A-11
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/functIon= "glucanase"
/product= "preprotein of the glucanase GluG"
                                                                                         1000 Agcrircegecricrica Accesaca Agrice ecesar Acaracaric 1050
                                                         961 AACTITIGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTC 1011
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LOCATION: 1083._1088
OTHER INFORMATION: /note= "potential polyadenylation signal"
                                                                                                                                                                                                                                                             Transgenic pathogen-resistant organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/138,873A

FILING DATE: August 24, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Tenser, Arthur

REGISTRATION NUMBER: 18,839

NAME: Kole, Lisa

REGISTRATION NUMBER: 35,225

REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335

TELECOMMUNICATION INVENTATION:

TELECOMMUNICATION INVENTATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                  Sequence 11, Application US/09138873A Patent No. 6271438 GENERAL INFORMATION:
                                                                                                                                                                                                                                                   TITLE OF INVENTION: Transgenic particle of SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Baker & Botts
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 765-2519
TELEX: 238555
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1235 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1235 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: polyA signal
LOCATION: 1210...1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1.48
FBAUTRE:
NAME/KRY: CDS
LOCATION: 49.1050
OTHER INFORMATION: //
OTHER INFORMATION: //
OTHER INFORMATION: //
FRAUTRE:
RAUTRE:
LOCATION: 1051.1235
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LOCATION: 1..48
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MOLECULE TYPE: c
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: L. FEATURE:
                                                                                                                                                   RESULT 6
US-09-138-873A-11
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288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 GCCCTCTCCGCGGCGCGCGCCCATCAAGGTGTCCACCTCCATCCGGTTCGACGAG 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 TACTICGCGIACCGIGACAACCCCGGGAGCATCAGCCTGAACTACGCGACGTICCAGCCG 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901 GAGACCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAAT 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            940 GAGACGTACATCTTCGCCATGTTCAACGAGAACCAGAAGACCGGGGACGCCACGGAGAGG 999
                                                                                                                                                                                                                                                                                                                                                                                   49 Ariescracaaaacarerrecerecarerrecagricererrerrearrecaerrecer 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 AACGAGGGGGGGGGGGCCCACGCGGAGCATCCTGCCGGCCATGCGCAACCTCAAACGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 GCAATCCCGAGAGGCGTGGAATCCATTGGGGTCTGCAATGGAATGGACGGTGACAACCTC
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                                                                                                                                                                                                                                                                                                                           4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCCTTGTAGTACTCTCG
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                                                                                                                                                                                                                                                                  Gaps
OTHER INFORMATION: /note= "potential polyadenylation signal" FEATURE:
                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                      Length 1235;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                   Query Match 30.8%; Score 346.2; DB 3; Best Local Similarity 60.4%; Pred. No. 2.1e-89; Matches 611; Conservative 0; Mismatches 388;
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389 AGTACGTCCTCCCAGCCATGAACAACATACAGTCCGCCCTCTCCTCTGCCGGCCTTCAGA 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545 GCACCGGAGCGCCGCTGCTGGTTAACGTGTACCCCTACTTCGCCTACGTCGGCGCGACACGA 604
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                                                                                                                                                                                          117 CGGGCGTCTCCTTCCGCTACATCGCCGTCGGCAACGAGGTCA---CCGGCGACGACGG
                                                                                                                                                                                                                                                                                                                            374 GCAACATCCTCCCGGCCATGAAGAACCTCAACGCCGGCGTCGGCGGCGGCGGCTCGGCG
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                                                                           257 GTTCGCCGCCGACGCCACCGCCGCCGCTCGGCTCAAGCAGAACGTCCAGGCCTACC
                                                                                                                                            CAAACGTTGCCTTCCGATACATCGCCGTCGGAAACGAAGTCATCCCCCGGCGCCCAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 GCGTCGGGGTGTCGTCCCAGGCGTGTCGCCAACTCCTACCCGCCTTCCA
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STREET: 350 Cambridge Ave., Suite
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09105390; Patent No. 6288303; GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: Rice Beta-Gluc; TITLE OF INVENTION: and Genes; NUMBER OF SEQUENCES: 66; CORRESPONDENCE ADDRESS: ADDRESSE: Dehlinger & Associate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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US-09-105-390-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTACAAGTCCAACAACATAGCTGCGACTCTACAGCCCCGACCAAGCCACTCTCC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGCCTCCAGGGCTCTAACATCTACCTCGACGTCCCCAACTCCGACCTCCAAA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCĄĘŢCACCGGCTCGAACATCGCCCTCACCATGGACGTCGCCAACGAGAACCTCGCCG 256
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                                              1000 AGCTTCGGGCTCTTCAACCCGGACAAGTCGCCGGCATACAACATCCAGTTC 1050
961 AACTITGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTC 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
29.4%; Score 330.6; DB 3; Length 996;
Best Local Similarity 61.4%; Pred. No. 6e-85;
Matches 607; Conservative 0; Mismatches 364; Indels 18;
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF EXQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSER: Delhinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLUM AND COMPUTER: IBM COMPAILLE COMPUTER: IBM COMPAILLE COMPUTER: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATE: US/09/105,390 FILING DATE: Filed herewith CLASSIFICATION NUMBER: US/09/105,390 FILING DATE: PAPLICATION DATE: APPLICATION NUMBER: 60/050,675 FILING DATE: 25-JUN-97 ATTORNEY/AGRIY, INFORMATION: NAME: Petithory, Joanne R. REGISTRATION NUMBER: P42,995 REFERENCE/DOCKET NUMBER: 2000-0455.30 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                  Sequence 57, Application US/09105390 Patent No. 6288303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Coding Sequence
LOCATION: 1...996
OTHER INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 996 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
FPATURE:
FFATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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US-09-105-390-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTCCGACCTCCAAAACATTGCCTCCGACCAATCCGCCGCCACCAACTGGGTCCAAACC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 AACGICCAAGCCIACCCAAACGIIGCCIICCGAIACAICGCCGICGGAAACGAAGTCAIC 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 AGAGGCGTGGAATCCATTGGGGTCTGCAATGGAATGGACGGTGACAACCTCCCCCAGCCC
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Pred. No. 3.7e-83;
0; Mismatches 340; Indels
SUPPRARE: FRASESEG for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY,AGENT INPORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REGISTRATION NUMBER: P42,995
REFREENCE/POCKET NUMBER: 2000-0455.30
TELEPHONE: 650-324-0880
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Best Local Similarity 62.1%;
Matches 587; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-324-0960
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US-09-105-390-5
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                                                                                                                                                            1939 GGGTGGCCGTCGGCGGTGGGGTTCGGGGCCGTGAGCAACGCGCAGAGCGTGACAACGT
730 TTGTACTCGGCCCTGGAGAGCGCCGGAGGCCCGAATGTCCCTGTTGTCGTGTCGGAGAGT 789
                                                                                                           GGCTGGCCGTCAGCGGGCGGGCACAGCGGCGACGTGTCTAATGCGCCAGACTTACAATTCC
                                                                                                                                                                                                                      850 AATTTGATCAACCATGTGGGTCAGGGGACGCCGAAGAGGCCAGG---GGCGGATTGAGACC
                                                                                                                                                                                                                                                                                                                                 TACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAATAACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            967 GGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTC 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2119 GGGCTGTTCAACCCAACAAGTCGCCGTCCTACAAATTAGATTC 2163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 41, Application US/09105390
Patent No. 6288303
GENERAL INFORMATION:
APPLICANT: Redriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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FILING DATE: Filed herewith
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-UNW-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REBERENCE/DOCKET NUMBER: 2000-0455.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
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STREET: 350 Cambridge Ave., Suite
CITY: Palo Alto
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TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Diskette
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OPERATING SYSTEM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
        NUMBER OF SEQUENCES:
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Patent No. 6288303
GENERAL INPORMATION:
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
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                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: DOS
SOFTWARE: FattERF for Windows Version 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
PRIOR APPLICATION:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Petithory, Joanne R.
RECISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
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APPLICATION NUMBR: 60/050,675
FILING DATE: 25-JTM-97
ATTORNEY/AGENT INFORMATION:
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CITER INFORMATION:
US-09-105-390-51
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STRANDEDNESS: single
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MEDIUM TYPE: Diskett
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                                       GATGCATCGTCGACATTCGGTCCAATCATACAGTTTCTAGCCAGCAATGGCTCCCCATTA 585
                                                                                                                                              TACGCCCTCTTTACTGCATCTGGTACAGTCGTACAGGACGGGTCCTAC---GCTTACAAC 702
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                                                                  CTTGCCAACATCTACCCCTACTTGAGCTATGCTGGCAACTCCGGATCCATCGACCTCTCA
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Sequence 2, Application US/09105390
Fatent No. 6288303
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
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REGISTRATION NUMBER: P42,995
REPERENCE/DOCKET NUMBER: 2000-0455.30
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APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN 97
ATTORNEY/AGENT INPORMATION:
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US-09-105-390-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCGACCTCCAAAACATTGCCTCCGACCAATCCGCCGCCACCAACTGGGTCCAAACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.6%; Score 310; DB 3; 60.4%; Pred. No. 7.4e-79;
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                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1949 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                571; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-09-105-390-2
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Best Local
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1844 GITCGCCATGITCAACGAGAACCAGAAGCCCGGGGAAGCCACGGAGCAAAACTITGGAGC 1903
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                             26.5%; Score 29%; DB 3; Length 918; 60.0%; Pred. No. 1.4e-75; ive 0; Mismatches 355; Indels 15;
                                                                                                                                            972 GITITACCCIAACGAACAGCCIGICIATICGAICAGCTICACTIGA 1017
                                                                                                                                                                                                                              Sequence 35. Application US/09105390

Patent No. 6288303
GENERAL INFORMATION:
APPLICANT: ROCITIGUEZ, RAYMOND
ITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
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APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY, AGENTY, INFORMATION:
NAME: Petithory, Joanne R.
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LOCATION: 1...918
OTHER INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM DISKETTE
OPERATING SYSTEM: DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 60.0
Matches 556; Conservative
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                                                                                                                                                                                                                                                                                                                    422 CCGGCGTGTTC------GCGGCGCCCTACATGACGGCCGTGGCCAAGCTCCTGCGAT 472
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182 ACCTCGCCGCCACCCGGCGTCCGCCGCGTCCTGGGTCGACGCGGAACGTCAAGCCGTTCG 241
                                       CAAACGTIGCCTICCGATACAICGCCGTCGGAAACGAAGTCAICCCCGGCGGCCCAAGCIC 388
                                                                                                                                                        302 AGAACATCCTCCCGGTCATGCAGAACATCAACGCCGCCCTGGCCGCGGCGGCGACCATCACCG 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 TCCCGGCGGTGAACATCAAGTACATCGCAACGAACGAGATCTCCGGCGAGCCCACGC
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Patent No. 6288303
GENERAL INFORMATION
TILLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      986 AACAGCCTGTCTATTCGATCAGCTTC 1011
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STATE: CA
COUNTRY:
ZIP: 943C
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Pred. No. 4e-72;
0; Mismatches 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESESEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  982 AACGAACAGCCTGTCTATTCGATCAGCTTC 1011
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 2000-045
REFERENCE/DOCKET NUMBER: 2000-045
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 59.8%;
Matches 562; Conservative C
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COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-324-0960
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                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAWE: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-324-0880
TELECHONE: 650-324-0980
   US/09/105,390
APPLICATION NUMBER: US/09/1.
FILING DATE: Filed herewith CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...996
OTHER INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS, single
TOPOLOGY: linear
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Best Local Similarity
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Associates

E: Dehlinger & Assoc 350 Cambridge Ave.,

Palo Alto

and

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NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
FITLE OF INVENTION:
                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94306
                                                                                                                                                 CITY: Pa]
STATE: C!
COUNTRY:
                                                                                                                       STREET:
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Sequence 37, Application US/09105390
Patent No. 6288303
GENERAL INFORMATION
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

RESULT 15 US-09-105-390-37

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                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: F881SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-UNA-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 82,995
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 59.5
Matches 552; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-324-0960
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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LOCATION: 1...909
COTHER INFORMATION:
US-09-105-390-37
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                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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526 CGCGACATCAGCCTCAACTACGCCACGTTCCGGCCGGGCACCACGGTGAGGGACCCAAAC 585
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        865
        GTGGGTCAGGGGAACGCCGAAGAGGCCAACGATTGAGACCTACATATTTGCCATGTTC
        924

        766
        GTGCGT---GGCACGCCCAAGAGGCGGGGGACTGGAGGCGTACATATTCGCCATGTTC
        822

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                             418 decidentricadadedecracardaadaacaredecidecadecar----- 466
                                                            568 AGCAATGGCTCCCCATTACTTGCCAACATCTACCCCTACTTGAGCTATGCTGGCAACTCC 627
                                                                          467 -GCACCGGGGGGCGCTGCTGCCCAACGTGTACCCGTACTTCGCCTACAGGGGAACCCG 525
                                                                                                                     628 GGATCCATCGACCTCTCATACGCCCTCTTTACTGCATCTGGTACAGT---CGTACAGGAC 684
                                                                                                                                                                              685 GGGTCCTACGCTTACAACAACCTCTTCGATGCCCATGGTCGACGCATTGTACTCGGCCCTG 744
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Search completed: April 7, 2006, 22:17:24 Job time : 247 secs.

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April 7, 2006, 20:50:38; Search time 1104 Seconds (without alignments) 8426.676 Million cell updates/sec
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1125
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1: /cgn2 6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2 6/ptodata/1/pubpna/USO9 PUBCOMB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO9A PUBCOMB.seq:*
4: /cgn2 6/ptodata/1/pubpna/USO9B PUBCOMB.seq:*
5: /cgn2 6/ptodata/1/pubpna/USLOB PUBCOMB.seq:*
6: /cgn2 6/ptodata/1/pubpna/USLOB PUBCOMB.seq:*
7: /cgn2 6/ptodata/1/pubpna/USLOB PUBCOMB.seq:*
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9: /cgn2 6/ptodata/1/pubpna/USLOB PUBCOMB.seq:*
10: /cgn2 6/ptodata/1/pubpna/USLOB PUBCOMB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9793542 segs, 4134689005 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                           OM nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description | Sequence 2, Appli Sequence 64217, Appli Sequence 6127, Appli Sequence 5107, Appli Sequence 14878, Aspli Sequence 14878, Appli Sequence 16329, A Sequence 16329, A Sequence 105, Appli Sequence 105, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 131, Appli Sequence 1313, Appli Sequence 8819, Appli |
|-------------------------------|---|
| SUMMARIES | US-10-647.649-2 US-10-447.963-64217 US-10-437-963-64217 US-10-849-2 US-10-849-2 US-10-739-930-5127 US-10-739-930-5127 US-10-767-701-14478 US-10-425-114-26408 US-10-425-114-26408 US-10-425-114-26408 US-10-425-114-26801 US-10-425-115-70439 US-10-425-115-70439 US-10-437-963-8819 US-10-437-963-8819 US-10-437-963-8819 US-10-437-963-8819 US-10-437-963-8819 US-10-437-963-8819 US-10-437-963-8819 US-10-437-963-8819 US-10-437-963-8819 |
| DB | 0 C B C B C C C C C C C C C C C C C C C |
| * Query Match Length DB | 1333 1439 1439 1633 1633 1633 1610 1110 1113 1120 1120 1209 1209 1209 1209 1209 1209 |
| & Query Match | 000 000 000 000 000 000 000 000 |
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| Sequence 8622, Ap | Sequence 75971, A | ٠. | 37. | Sequence 75976, A | Sequence 8818, Ap | | Sequence 28299, A | Sequence 33684, A | Sequence 15488, A | Sequence 15621, A | Sequence 109294, | Sequence 8822, Ap | 17839, | CA | Sequence 23200, A | Sequence 82368, A | Sequence 27807, A | ٠. | Sequence 51614, A | Sequence 736, App | Sequence 33997. A |
|--------------------|---------------------|-------------------|------------------|---------------------|--------------------|----------------------|---------------------|---------------------|---------------------|---------------------|----------------------|--------------------|--------------------|---------------------|--------------------|---------------------|---------------------|--------------------|---------------------|-------------------|---------------------|
| | | Ze Se | Se | - | | | | | | | 94 | | 6 | | 0 | | | _ | _ | | |
| US-10-437-963-8622 | US-10-437-963-75971 | US-10-259-165-377 | US-10-259-165-37 | US-10-437-963-75976 | US-10-437-963-8818 | US-10-425-115-173325 | US-10-425-114-28299 | US-10-437-963-33684 | US-10-767-701-15488 | US-10-767-701-15621 | US-10-425-115-109294 | US-10-437-963-8822 | US-10-437-963-1783 | US-10-425-114-23140 | US-10-425-114-2320 | US-10-437-963-82368 | US-10-425-114-27807 | US-10-425-114-3175 | US-10-425-115-51614 | US-10-259-165-736 | US-10-425-114-33997 |
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| 2466 | 1088 | 954 | 957 | 1319 | 1174 | 1308 | 1228 | 1218 | 1919 | 1358 | 1262 | 1899 | 1022 | 1245 | 1249 | 2324 | 1261 | 1204 | 2094 | 1017 | 1138 |
| 29.5 | 29.0 | 28.9 | 28.9 | 28.9 | 28.9 | 28.5 | 28.4 | 28.0 | 27.9 | 27.8 | 27.5 | 27.0 | 27.0 | 26.8 | 26.8 | 26.7 | 26.3 | 26.1 | 26.1 | 26.0 | 25.9 |
| 329 | 326.8 | 325.6 | 325.6 | 325.2 | 325 | 320.6 | 319 | 314.6 | 314.4 | 313 | 309 | 304.2 | 303.8 | 301.6 | 301.6 | 300.2 | 296 | 293.4 | 293.4 | 292.4 | 291.6 |
| 24 | 52 | 56 | 27 | 28 | 59 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

RESULT 1 US-10-647-649-2 Sequence 2, Application US/10647649 ; Publication No. US20050048638A1

123

228 183 288 243 348

168

63

303 408 468

363

525

483

423

585

543 633 603 693 663 753 723 813 783 873 843 933 903

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904 ACCIACAIAITIGCCAIGIICAACGAGGAICAGAAGCAGCCGCAAGGGAIIGAGAAIAAC 963
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                                                                                                                                                                                                                                        18;
                                                                                                                                                                                        Length 1333,
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                     4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCCT
                                                                                                                                                                                           Score 431.4; DB 7;
Pred. No. 3.8e-124;
                                                                                                                                                                                                                                     0; Mismatches 321;
                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_65383C.1
US-10-437-963-64217
                                                                                                                                                                                      38.3%;
                                                                                                                                                                                        Query Match
Best Local Similarity 66.8
Matches 682; Conservative
SEQ ID NO 64217
LENGTH: 1333
TYPE: DNA
ORGANISM: OFYZA BATIVA
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shou, Yilua
APPLICANT: Cao, Yongwel
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT: May, Gregory D.
APPLICANT: May, Gregory D.
APPLICANT: Mason, Hugh S.
APPLICANT: Arntzen, Charles J.
TITLE OF INVENTION: DNA Regulatory Elements Associated with Fruit Development
FILE REFERENCE: 031998-007
CURRENT APPLICATION NUMBER: US/09/892,635A
CURRENT PLING DATE: 2001-06-28
PRIOR PILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 45

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSEQ for Windows Version 4.0
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              ; Sequence 17, Application US/09892635A; Publication No. US20030226175A1
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OTHER INFORMATION: Complement
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Matches 670; Conservative
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US-09-892-635A-17
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LENGTH: 3559
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Publication No. US20040216190A1

GENERAL INFORMATION:
APPLICANT: KOVALIC.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
FILE REPERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT APPLICATION NUMBER: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 5127
TTTGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTCACTTGAGAAATT 1023
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                                                                                                                                                                                             OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER494_2
                                                                                                                                                                                                                                                    Score 394.2; DB 8;
Pred. No. 2e-112;
0; Mismatches 328;
TITLE OF INVENTION: PLANTS AND USES THEREOF FILE REFERENCE: 38-21(5337)B CURRENT APPLICATION NUMBER: US/10/739,930 CURRENT FILING DATE: 2003-12-18 NUMBER OF SEQ ID NOS: 11088 SEQ ID NOS: 11488
                                                                                                                                                                                                                                                        35.0%;
                                                                                                                                       TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
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Best Local Similarity 64.9'
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S-10-739-930-5007
Sequence 5007, Application US/10739930
Sublication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Rovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

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GCGCCCATCGCGCAGTACCTGCAGAGCACGGGGCCCCCGCTGCTCTGCAACGTCTACCCC
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Pred. No. 1.7e-109;
0; Mismatches 357;
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US-10-425-115-67183
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Matches 631; Conservative
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ORGANISM: Zea mays
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US-10-425-115-67183
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                                                                                                                                                   Sequence 14818, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongweichen Nucleichen Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REPERENCE: 38-21 (53535) B CURRENT PLING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 14878

LENGTH: 1633
                   945 CTCCATGTTCAACGAGAACGAGAAGGA---CAGCGGCGTGGAGGAGAACTGGGGACTCTT 1001
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915 TGCCAFGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAATAACTTTGGGCTGTT
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                                                                               1002 CTACCCCAACATGCAGGACGTCTACCCCATCAGCTTCTGATGAGGTAGCTG 1052
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US-10-767-701-14878
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Pred. No. 6.7e-112;
0; Mismatches 359;
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Best Local Similarity 63.2%;
Matches 643; Conservative
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                                                                                                                                         US-10-767-701-14878
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Sequence 67183, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: APPLICANT: Thomas J.
APPLICANT: APPLICANT: Ano. Yihua
APPLICANT: APPLICANT: Ano. Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 30-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
UNDER OF SEQ ID NOS: 369326
SEQ ID NO 67183
ELENGTH: 1410 783 843 306 366 257 426 663 751 811 GACACCTTCGTGTCCGCGCTCGAGAACGCCGGGAACGTCGGCGTCGTCGTCGTCCTCC 871 GAGAGCGGCTGGCCGTCCGCCGCGGCGACGCCGCCACGCCGGGGAACGCGCAGACCTAC 931 AATTCCAATTTGATCAACCATGTGGGTCAGGGGACGCCGAAGAGGCCAGGGGCGATTGAG 903 ACCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAGAATAAC 963 246 137 138 GGTCGTCAACTCTACAAGTCCAACAAAAATAGCTGGCATGCGACTCTACAGCCCCGACCA 197 77 TTCGGACTCTTCAACCCGGACAAATCGCCGGCGTACTCCCATCAATTTCTCTCTAAAAA 1108 TITGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTCACTTGAGAA 1020 752 CCGGGGACCGTCGTCGTGCACGCACGCGTACCAGAACCTCTTCGACGCGCTCGTC GACGCATTGTACTCGGCCCCTGGAGGCGCCGGAGGGCCGAATGTCCCTGTTGTCGTGT GAGAGTGGCTGGCCGGCGGGGGACAGCGGCGACGGTGTCTAATGCGCAGACTTAC TACTICTCCTACACGGGGAACGAGGCCCAGATCGCCCCTCAGCTACGCGCGCTCTTCACGTCG TACTTGAGCTATGCTGGCAACTCCGGATCCATCGACCTCTCATACGCCCTCTTTACTGCA TCTGGTACAGTCGTACAGGACGGGTCCTACGCTTACAACAACCTCTTCGATGCCATGGTC 247 AGTCCAATCGACGTGTGTGCTACGGCGTGAACGGCGACAACCTGCCCCCGGGGAGGA 187 cercecriccarecercecratecricitations de la contractation de la contractación de la CGTGGAATCCATTGGGGTCTGCAATGGAATGGACGGTGACAACCTCCCCCAGCCCGCGA 198 AGCCACTCCAGGCCCTCCAGGCTCTAACATCTACCTCCATCCTCGACGTCCCCAACTC 18 CATCATCTCCATGCCTGCCATGCCATCCCTCCTTGTAGTACTCTCGGCAATCCCGAGAGG Gaps Indels 12; Length 1410;

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TYPE: DNA
ORGANISM: Zea mays
PEATURE:
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                                                                                                         Query Match
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Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Lit, Jingdong

APPLICANT: Soreen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: DATE: 2003-04-28

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

SEQ ID NO 26408

LENGTH: 1268
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                                                                                                                                                                                                                                      Length 1268,
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                                                                                                                                                                                                                                      Score 381.6; DB 7;
Pred. No. 1.7e-108;
                                                                                                                                                                                                                                                                                                                       0; Mismatches 359;
; TYPE: DNA
; ORGANISM: Zea maye
; PEATURE:
; OTHER INFORMATION: Clone ID: LIB4172-007-A12_FLI
US-10-425-114-26408
                                                                                                                                                                                                                                      33.9%;
62.9%;
                                                                                                                                                                                                                                                                                                                            Matches 629; Conservative
                                                                                                                                                                                                                                                                                     Local Similarity
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APPLICANT: Expension:
APPLICANT: Expension:
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bucharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICANTON NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 97429
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                                                       AcGCCCATCGCGAGTACCTGGCGAGCACCGGCGCGCCGCTGATGGCCAACGTCTACCCC
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Best Local Similarity 60.8%; Pred. No. 3.5e-100;
Matches 616; Conservative 0; Mismatches 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_95433C.1
US-10-437-963-97429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 97429, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
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                                                                                                                                                                                                     Joseph Hard Sequence 16329, Application US/10437963

j Publication No. US20040123343A1

j Publication No. US20040123343A1

j GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yihua
    APPLICANT: Cao, Yongwei
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Buckharov, Andrey A.
    APPLICANT: Buckharov, Andrey A.
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Rice Nucleic Acid Molecules Associated With
    TITLE OF INVENTION: Rice Nucleic Acid Molecules Associated With
    TITLE OF ENERGY APPLICANTON NUMBER: US/10/437, 963

    CURRENT FILING DATE: 2003-05-14
    NUMBER OF SEQ ID NOS: 204966
    SEQ ID NO 16329
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Pred. No. 8.8e-104;
0; Mismatches 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT4530_22088C.1
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Best Local Similarity 61.5%;
Matches 624; Conservative (
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                                                                                                                                                                RESULT 9
US-10-437-963-16329
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US-10-437-963-16329
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APPLICANT: Nicholas
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APPLICANT: Ricke, Darrell
TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REFERENCE: 70030-NP
CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT FILING DATE: 2002-09-26
PRIOR PILING DATE: 2002-09-04
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-03-27
PRIOR RILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 782
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US-10-259-165-439/C
; Sequence 439, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
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                                                                                                                          ATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCCTTGTAGTACTCTCG
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                                                                                       Gaps
                                                                                       9
                                                   Length 1110;
                                                                                       IndelB
                                                   Score 354.2; DB 6;
Pred. No. 6.3e-100;
0; Mismatches 388;
                                                  31.5%;
                                                31.5°
Best Local Similarity 60.9°
Matches 613; Conservative
; ORGANISM: Oryza sativa
US-10-259-165-439
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwel
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
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                                              GAAGTCATCCCCGGCGCCAAGCTCAGTACGTCCTCCCAGCCATGAACATACAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 GCGCCCGTCCTGAGCTTCCTCGCCCGCACCGCCGCCGCCTGCTCGCCCAACATCTACCCC
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TACAGCCCCGACCAAGCCACTCTCCAGGCCCTCCAGGCCTCTAACATCTACCTCCATCCTC
                                                                                               244 GACGICCCCAACTCCGACCICCAAACATTGCCTCCGACCAATCCGCCGCCACCAACTGG
                                                                                                                                                                                              GTCCAAACCAACGTCCAAGCCTACCCAAACGTTGCCTTCCGATACATCGCCGTCGGAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-425-114-20801
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APPLICANT: Glazebrook, Jane
APPLICANT: Ratagiri, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Moughamer, Todd
APPLICANT: Provart, Nicholas
APPLICANT: Provart, Nicholas
APPLICANT: Provart, Nicholas
APPLICANT: Price, Darrell
TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REPERENCE: 10010-09-26
FRIOR PRICATION NUMBER: US 60/370,620
FRIOR PRILING DATE: 2002-09-26
FRIOR PRILING DATE: 2002-09-26
FRIOR PRILING DATE: 2002-09-26
FRIOR APPLICATION NUMBER: US 60/325,277
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                                                           GACGCGTTCTACGCCGCCATGGCCAAGCACGGCTCCGGCGTCTCCCTCGTCGTCTCC 253
                                                                                                                   843
                                                                                                                                                             GAGACAGGCTGGCCTCCGCCGGCGCATGTCCGCCTCGCCGGCCAACGCCCGGATCTAC 193
                                                                                                                                                                                                                                          ACCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCCAAGGGATTGAGAATAAC 963
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                                                                                                              GAGAGTGGCTGGCCGTCAGCGGCGGGACAGCGGCGACGGTGTCTAATGCGCAGACTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 105, Application US/10259165
Publication No. US20030135888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang, Xun
Chang, Hur-song
Briggs, Steven P.
Cooper, Bret
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; ORGANISM: Oryza Bativa
US-10-259-165-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 615; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhu, Tong
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TYPE: DNA ORGANISM: Zea mays
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Pred. No. 3.6e-98;
0; Mismatches 317;
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                                                                                                                                                                                                     31.0%;
al Similarity 64.1%;
597; Conservative
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 20801
LENGTH: 1464
                                                                                                                                    ; OTHER INFORMATION:
US-10-425-114-20801
                                                                     TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Tovalic, David K.
APPLICANT: Zhou, Yihus
APPLICANT: Zao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
LENGTH: 1464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 ACAGITICTAGCCAGCAATGGCTCCCCATTACTTGCCAACATCTACCCCTACTTGAGCTA
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Pred. No. 3.6e-98;
0; Mismatches 317;
940
                                                                                                986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: MRT4577_16422C.1
US-10-425-115-70439
     CATATTTGCCATGTTCAACGAGGATCAGAAGC
                                                                    ; Sequence 70439, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 64.1%;
Matches 597; Conservative
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49 ATGGCTAGAAAGATGTTGCCTCCATGTTTGCAGTTGCTCTTTCATTGGAGCATTGGCT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dererrecraegadrerecarecearececerarecraegecraegerececaacaacare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGTCCCCAACTCCGACCTCCAAACATTGCCTCCGACCAATCCGCCGCCACCAACTGG 303
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                                                                       OTHER INFORMATION: /codon start= 49
OTHER INFORMATION: /function= "glucanase"
OTHER INFORMATION: /function= "glucanase"
OTHER INFORMATION: /product= "preprotein of the glucanase GluG"
FRATURE: 1051..135
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "14 nucleotides at the 3'end not shown."
NAME/KEY: polyA signal
LOCATION: 1083..1088
OTHER INFORMATION: /note= "potential polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCCTTGTAGTACTCTCG
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LOCATION: 1210._1215
OTHER INFORMATION: /note= "potential polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
30.8%; Score 346.2; DB 3; Length 1235;
Best Local Similarity 60.4%; Pred. No. 2.2e-97;
Matches 611; Conservative 0; Mismatches 388; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mat peptide LOCATION: 133..1050
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US-09-138-873A-11
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729 ATTGTACTCGGCCCTGGAGGCGCCGGAGGCCGAATGTCCCTGTTGTCGTCTCGGGAGG 788
                                                                                                                                                                          ----GICGIACAGGACGGGICCTACGCTTACAACAACCTTCGATGCCATGGTCGACGC 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                789 TGGCTGGCCGTCAGCGGGGGGGACAGCGGCGACGTGTTAATGCGCAGACTTACAATTC 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             849 CAATTTGATCAACCATGTGGGTCAGGGACGCCGAAGAGGCCCAGGGGCGATTGAGACCTA 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             895 GAACCTCATCAACCACGTCGGCCAGGGCACCCGAAGCCCCCGGGCCCGATAGAGGCCTA 954
                                                                                                                                                                                                                                                       715 GETGGTGGTGCAAGACGGCGGCTACGACTACGACTGCCTGTTCGATGCGATGGTCGACTG
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

CONFUTER: FLOPPY disk
CONFUTER: IBM FOC COMPACTION

COREATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPC
CURENT APPLICATION DATA:

APPLICATION NUMBER: US/09/138,873A

FILING DATE: August 24, 1998

ATORNEY/AGENT INFORMATION:

NAME: Tenser, Arthur

REGISFATION NUMBER: 18,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - 37/31335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              955 CATATTCGCCACGTTCAACGAGGACCAGAAGC 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISITATION TO THE STATE OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09138873A Publication No. US20010020300A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Baker & Botts
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1235 base pairs
TYPE: nucleic acid
STRANDEDNESSE: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..48
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NAME/KEY:
LOCATION:
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US-09-138-873A-11
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961 AACTTTGGGCTGTTTTACCCTAACGAACAGCCTGTCTATTCGATCAGCTTC 1011
1010 AGCTTCGGGCTCTTCAACCCGGACAAGTCGCCGGCATACAACATCCAGTTC 1050
6 8 6 8 6 8 6
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Search completed: April 7, 2006, 22:35:54 Job time : 1109 secs

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April 7, 2006, 20:54:59; Search time 661 Seconds (without alignments) 6808.813 Million cell updates/sec
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19: /SIDSS/ptodata/1/pubpna/USII_NEW_PUB.seq:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery No. Score Match Length DB ID Description

No. Score Match Length DB ID Description

| 1 86.2 7.7 438 | 11 US-11-116-881A-189 | Sequence 1842, Apple 2 86.2 7.7 491 | 11 US-11-116-881A-2189 | Sequence 2189, Apple 3 86.2 7.7 491 | 11 US-11-116-881A-1704 | Sequence 2189, Apple 4 80.8 7.2 386 | 11 US-11-116-881A-1704 | Sequence 2132, Apple 6 55.6 4.9 1330 | 14 US-11-116-881A-1704 | Sequence 1232, Apple 6 55.6 4.9 1330 | 14 US-11-118-891-16 | Sequence 1231, Apple 10 48.2 4.3 6645 | 14 US-11-128-061-426 | Sequence 426, Apple 10 48.2 4.3 6645 | 14 US-11-128-049-426 | Sequence 426, Apple 11 47.2 4.2 3486 9 US-10-932-182A-191019 | Sequence 191019, 13 47.2 4.2 88421 | 11 US-11-128-061-426 | Sequence 191019, 14 4.2 142303 | 14 US-11-121-086-42 | Sequence 52, Apple 16 46.8 4.2 6210 | 14 US-11-121-086-42 | Sequence 53, Apple 17 46.8 4.2 6210 | 14 US-11-121-086-42 | Sequence 53, Apple 18 46.8 4.2 6210 | 14 US-11-121-086-42 | Sequence 538, Apple 18 46.8 4.2 6210 | 14 US-11-052-554A-538 | Sequence 518, Apple 18 46.8 4.2 6210 | 14 US-11-052-554A-538 | Sequence 518, Apple 19 46.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 46.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 14 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 | 4 US-11-052-554A-518 | Sequence 518, Apple 19 40.8 4.2 6210 |

7.7%; Score 86.2; DB 11; Length 438;

TYPE: DNA ORGANISM: Nicotiana tabacum

SEQ ID NO 1842

US-11-116-881A-1842

Query Match

| | υ | 19 20 21 | 45.8 5.8 6.7 | 444 | 1108 4983 | ਜਜਜ | US-11-0 US-11-0 | 96-568A-1128 52-554A-521 18-780-5 | 8 | Sequence | 11282, 7 521, Ap |
|--|------------|-------------------|--------------------|------------------------|-----------|---------|--------------------|---|-------|-----------|---------------------|
| 25 446 40 186 11 105-11-107-881A-1895 Sequence 25 44 3:9 1326 8 105-11-107-855-19 Sequence 26 44 3:9 1326 8 105-11-107-855-19 Sequence 26 43.8 3:9 137 11 10 11-1025-65-1-3 Sequence 27 43.8 3:9 137 11 10 11-1025-65-1-3 Sequence 28 43.8 3:9 1473 11 10 11-1025-65-1-3 Sequence 29 43.8 3:9 1473 11 10 11-1025-65-1-3 Sequence 29 43.8 3:9 1473 11 10 11-102-85-1-5-1-5 Sequence 23 43.2 3.8 2010 14 US-11-208-659-17 Sequence 23 43.2 3.8 2010 14 US-11-208-659-17 Sequence 24 43.2 3.8 2010 14 US-11-208-659-17 Sequence 24 43.3 3.8 1613 14 US-11-008-568-1655 Sequence 24 43.3 3.8 1613 14 US-11-008-568-1655 Sequence 24 43.3 3.8 1613 14 US-11-008-568-1655 Sequence 24 43.3 3.8 1613 14 US-11-008-568-1657 Sequence 24 43.3 3.8 1613 14 US-11-008-568-1657 Sequence 24 42.6 3.8 1741 11 US-11-008-568-1657 Sequence 24 42.6 3.8 1741 11 US-11-008-568-1657 Sequence 24 42.2 3.8 1741 11 US-11-008-568-1557 Sequence 24 42.2 3.7 1450 11 US-11-008-568-1557 Sequence 24 42.2 3.8 1570 14 US-11-008-568-1557 Sequence 24 42.2 3.7 1450 11 US-11-008-568-1557 Sequence 24 42.2 3.8 1570 14 US-11-008-568-1557 Sequence 24 42.2 3.7 1450 US-11-008-568-1557 Sequence 24 42.2 3.8 1570 US | | 22 | | 4.4 | 1583 | 1 77 7 | US-11-0 | 96-568A-1250 | _ | Sequence | 12501, |
| 25 44 3.9 120 8 US-10-525-64-55 Sequence 27 44.8 3.9 1157 11 US-11-005-568-21483 Sequence 28 44.8 3.9 1167 11 US-11-105-568-519 Sequence 29 43.8 3.9 1167 11 US-11-105-554-548 Sequence 31 43.2 3.8 210 14 US-11-228-559-17 Sequence 32 43.2 3.8 210 14 US-11-28-559-17 Sequence 33 43.2 3.8 210 14 US-11-058-275 Sequence 34 43.2 3.8 210 14 US-11-058-275 Sequence 35 43.2 3.8 210 14 US-11-058-275 Sequence 36 43 3.8 1613 14 US-11-058-554-539 Sequence 36 43 3.8 1613 14 US-11-056-568-11655 Sequence 36 43 3.8 1513 14 US-11-056-568-11655 Sequence 36 42.6 3.8 1379 11 US-11-056-568-11670 Sequence 37 42.5 3.8 1379 11 US-11-056-568-11670 Sequence 38 42.6 3.8 1379 11 US-11-056-568-11489 Sequence 38 42.6 3.8 1379 11 US-11-056-568-11489 Sequence 41 42.2 3.8 4581 9 US-10-932-511-137-5 Sequence 42 42.2 3.8 4581 9 US-10-932-511-137-5 Sequence 43 41.8 3.7 1191 11 US-11-056-568-12670 Sequence 44 41.8 3.7 1191 11 US-11-066-568-12670 Sequence 45 41.8 3.7 1450 11 US-11-066-568-12670 Sequence 46 41.8 3.7 1450 11 US-11-066-568-12512 Sequence 47 41.8 3.7 1450 11 US-11-066-568-12512 Sequence 48 41.8 3.7 1450 11 US-11-066-568-12512 Sequence 49 41.8 3.7 1450 11 US-11-066-568-12512 Sequence 40 82.05000041349A1 41.11 Septimental 4 | υ | 24 | . 4 | ٠. | 386 | i | US-11-1 | 16-881A-1385 | | Sequence | 1385, A |
| 28 43.8 3.9 1731 11 03-11-09-29-39 Sequent 23 43.8 3.9 1731 11 03-11-002-354-39 Sequent 33 43.8 3.9 1731 11 03-11-002-354-39 Sequent 33 43.8 3.9 1731 11 03-11-002-354-39 Sequent 34 43.2 3.8 2010 14 03-11-28-259-17 Sequent 35 43.2 3.8 2010 14 03-11-28-25-3-5 Sequent 35 43.2 3.8 2010 14 03-11-28-25-3-5 Sequent 35 43.2 3.8 2010 14 03-11-28-25-3-5 Sequent 35 43.2 3.8 1313 11 03-11-06-58-31-3 Sequent 35 43.2 3.8 1313 11 03-11-06-58-31-3 Sequent 37 43.2 3.8 1313 11 03-11-06-58-31-33 Sequent 39 42.6 3.8 1737 11 03-11-06-584-155 Sequent 39 42.6 3.8 1737 11 03-11-06-584-139 Sequent 40 42.2 3.8 1737 11 03-11-06-584-137 Sequent 41 42.2 3.8 1737 11 03-11-06-584-1349 Sequent 41 42.2 3.8 1737 11 03-11-06-584-1349 Sequent 41 42.2 3.8 1737 11 03-11-06-584-1349 Sequent 41 42.2 3.8 1737 11 03-11-06-584-1347 Sequent 41 42.2 3.8 1737 11 03-11-06-584-1347 Sequent 42 41.8 3.7 1450 11 03-11-06-584-1251 Sequent 43 42.6 3.8 1737 11 03-11-06-584-1251 Sequent 44 41.8 3.7 1450 11 03-11-06-584-1251 Sequent 45 41.8 3.7 1450 14 03-11-06-584-1251 Sequent 45 41.8 3.7 1440 14 03-11-06-584-1251 Sequent 45 03-106-584-1251 Sequent 45 03-106-584-1251 Sequent 45 03-106-584-1251 Sequent 45 03- | | 25 | | • | 1296 | ω, | US-10-52 | 5-674-25 | | Sequence | 25, Appl |
| 28 43.8 3.9 1167 11 US-11-228-659-19 Sequent 31 43.2 3.9 3419 11 US-11-228-659-17 Sequent 32 43.8 3.9 3419 11 US-11-228-659-17 Sequent 33 43.2 3.8 2010 14 US-11-228-659-17 Sequent 34 43.2 3.8 2010 14 US-11-228-659-17 Sequent 35 43.2 3.8 2010 14 US-11-08-5684-1655 Sequent 37 42.6 3.8 10.01 14 US-11-08-5684-1655 Sequent 37 42.6 3.8 10.01 14 US-11-08-5684-1670 Sequent 39 42.6 3.8 1379 11 US-11-08-5684-1670 Sequent 42.2 3.8 1379 11 US-11-08-5684-1670 Sequent 42.2 3.8 1379 11 US-11-09-5684-1670 Sequent 42.2 3.8 1370 11 US-11-09-5684-1670 Sequent 44 41.8 3.7 1191 11 US-11-09-5684-1670 Sequent 44 41.8 3.7 1191 11 US-11-09-5684-1670 Sequent 44 41.8 3.7 1450 11 US-11-08-5684-1512 Sequent 44 41.8 3.7 1450 11 US-11-08-5684-1512 Sequent 44 41.8 3.7 1450 11 US-11-08-5684-1512 Sequent 45 41.8 3.7 1450 11 US-11-08-5684-1512 Sequent 45 41.8 3.7 1450 11 US-11-08-5684-1512 Sequent 500-50-30-30 Sequent 500-50-30 Sequent | | 27 | | | 773 | i | US-11-1 | 36-366A-2148 | • | Sequence | 3. Appl |
| 29 43.8 3.9 1731 14 US-11-052-659-77 Sequent 31 43.2 3.8 2.010 14 US-11-220-659-77 Sequent 32 43.2 3.8 2.010 14 US-11-220-659-77 Sequent 32 43.2 3.8 2.010 14 US-11-056-558-77 Sequent 32 43.2 3.8 2.010 14 US-11-056-568-1655 Sequent 32 43.2 3.8 2.010 14 US-11-056-568-1655 Sequent 32 43.2 3.8 2.010 14 US-11-056-568-1657 Sequent 32 43.2 3.8 1.010 14 US-11-056-568-1657 Sequent 32 42.6 3.8 1.010 14 US-11-056-568-1657 Sequent 32 42.6 3.8 1.010 14 US-11-056-568-1369 Sequent 32 42.6 3.8 1.010 14 US-11-056-568-1369 Sequent 40 42.2 3.8 1.010 14 US-11-056-568-1369 Sequent 40 42.2 3.8 1.010 14 US-11-056-568-1369 Sequent 41 42.2 3.8 1.010 14 US-11-056-568-1369 Sequent 42 2 3.8 1.010 14 US-11-056-568-1369 Sequent 43 3.7 1.010 14 US-11-056-568-1369 Sequent 44 1.8 3.7 1.01 14 US-11-056-568-12512 Sequent 43 3.7 1.010 14 US-11-056-568-12512 Sequent 45 41.8 3.7 1.010 14 US-11-056-568-12512 Sequent 54 US-11-056-568 | | 28 | • | • | 1167 | H | US-11-2 | 28-659-19 | | Sequence | 19, App |
| 32 43.2 3.9 31.1 105.110.85.72.5 Sequence 3.4 43.2 3.8 2010 14 US-111-08-189-5 Sequence 3.4 43.2 3.8 2010 14 US-111-08-189-5 Sequence 3.4 43.2 3.8 2010 14 US-111-08-189-5 Sequence 3.4 43.2 3.8 2010 14 US-11-03-5.84-53 Sequence 3.4 43.3 3.8 12.8 14.8 11 US-11-03-5.84-53 Sequence 3.8 42.6 3.8 1741 11 US-11-03-5.84-53 Sequence 4.2 5.8 3.8 1741 11 US-11-03-5.84-53 Sequence 4.4 2.3 3.8 1741 11 US-11-03-5.84-7947 Sequence 4.4 2.3 3.8 1772 11 US-11-03-5.84-7947 Sequence 4.4 2.3 3.8 1772 11 US-11-03-5.84-7947 Sequence 4.4 2.3 3.8 1772 11 US-11-03-184-7947 Sequence 4.4 2.3 3.8 1772 11 US-11-03-184-7947 Sequence 4.4 3.8 3.7 1250 14 US-11-10-17-10.8 Sequence 4.4 3.8 3.7 1250 14 US-11-03-184-7947 Sequence 5.4 2 3.8 17.8 11 US-11-03-5.84-53 Sequence 4.4 3.8 3.7 1250 14 US-11-03-184-7947 Sequence 5.4 2 3.7 2250 14 US-11-03-184-7947 Sequence 5.4 2 3.7 2250 14 US-11-03-5.84-53 Sequence 6.4 2 3.7 2250 14 US-11-03-5.84-53 Sequence 6.4 2 3.7 2250 14 US-11-03-5.84-53 Sequence 7.4 1.8 3.7 1450 11 US-11-03-5.84-73 Sequence 7.4 1.8 3.7 140 Sequence 7.4 1.8 3.7 140 Sequence 7.4 1.8 3.7 140 Sequenc | υ | 5 6 | | • | 1731 | à, | US-11-0 | 52-554A-548 | | Sequence | 548, Ap |
| 32 43.2 3.8 2010 14 US-11-216-595-5 Sequent 34 43.2 3.8 2010 14 US-11-246-65-5 Sequent 35 43.2 3.8 2010 14 US-11-246-65-5 Sequent 36 43 3.8 1613 14 US-11-026-586A-1655 Sequent 37 42.6 3.8 1613 14 US-11-026-586A-1670 Sequent 39 42.6 3.8 1741 11 US-11-055-56A-1670 Sequent 39 42.6 3.8 1741 11 US-11-055-56A-1670 Sequent 42.2 3.8 4581 9 US-10-392-18A-7943 Sequence 14 42.2 3.8 4581 9 US-10-392-18A-7943 Sequence 42.2 3.8 4581 9 US-10-392-18A-7943 Sequence 42.2 3.8 4581 9 US-10-392-18A-7943 Sequence 44 41.8 3.7 1191 11 US-11-055-56A-25594 Sequence 15 42.2 3.8 15720 14 US-11-055-56A-25594 Sequence 16 42.2 40.2 40.2 40.2 40.2 40.2 40.2 40.2 | | 31 | | | 2010 | -i - | US-11-2 | 58-53-17 | | Sequence | II, App |
| 33 43.2 3.8 2010 14 US-11-224-624-55 Sequence | | 32 | | | 2010 | iÀ | US-11-1 | 08-389-5 | | Sequence | 5. Appl |
| 34 43.2 3.8 2135 11 US-11-036-568A-11655 Sequence 35 43 3.8 1613 14 US-11-024-959-71 Sequence 36 43 3.8 1513 14 US-11-024-959-71 Sequence 37 42.6 3.8 1525 14 US-11-024-958-733 Sequence 38 42.6 3.8 1793 11 US-11-095-568A-13275 Sequence 42.2 3.8 4581 9 US-10-995-561-13275 Sequence 42.2 3.8 4581 9 US-10-995-561-13275 Sequence 42.2 3.8 4581 9 US-10-995-561-13275 Sequence 42.2 3.8 4581 9 US-10-932-188A-79437 Sequence 42.2 3.8 15220 14 US-11-108-172-1058 Sequence 42.2 3.7 120 11 US-11-096-568A-2569 Sequence 43 3.7 120 11 US-11-096-568A-2569 Sequence 44 41.8 3.7 1191 11 US-11-096-568A-2569 Sequence 45 41.8 3.7 1191 11 US-11-096-568A-2569 Sequence 45 41.8 3.7 1450 11 US-11-096-568A-2569 Sequence 45 APPLICANT NUMBER: 05/665,451 Sequence 45 APPLICANT NUMBER: 05/665,451 Sequence 46 ENGREY PERIOR DATE: 2005-04-27 Sequence 47 APPLICANTON NUMBER: 05/665,997 Sequence 48 PRIOR APPLICATION NUMBER: 05/665,997 SPRIOR PELING DATE: 2005-04-27 Sequence 48 PRIOR APPLICATION NUMBER: 06/665,451 SPRIOR APPLICATION NUMBER: 06/66,454 SPRIOR APPLICATION NUMBER: 06/66,454 SPRIOR APPLICATION NUMBER: 06/66,454 SPRIOR APPLICATION NUMBER: 06/66,454 SPRIOR APPLICATION NUMBER: 06/66,355 SPRIOR PILING DATE: 2005-04-27 SPRIOR APPLICATION NUMBER: 06/66,356 SPRIOR PILING DATE: 2006-09-30 SPRIOR PILING DATE: 2006-09 | | 33 | | • | 2010 | Ä | US-11-2 | 24-624-5 | | Sequence | 5, Appl |
| 35 43 3.8 1613 14 US-11024-558-71 Sequent 43 42.6 3.8 1379 11 US-11056-5684-16670 Sequent 42.6 3.8 1379 11 US-110-095-5684-16670 Sequent 42.6 3.8 1379 11 US-110-095-5684-16670 Sequent 42.2 3.8 14581 9 US-10-932-1824-79437 Sequence 44.2 4.2 3.8 4581 9 US-10-932-1824-79437 Sequence 42.2 3.8 4581 9 US-10-932-1824-79437 Sequence 42.2 3.8 15720 14 US-11-096-5684-12512 Sequence 42.2 3.8 15720 14 US-11-108-172-1058 Sequence 43.7 1292 18 15720 14 US-11-096-5684-12512 Sequence 18.2 3.7 2520 14 US-11-06-5684-12512 Sequence 18.2 3.7 205-04-27 Sequence 18.2 3.2 3.2 3.2 3.2 3.2 3. | | ۳ ر م | | • | 2135 | ∺, | US-11-0 | 96-568A-1165 | | Sequence | 11655, |
| 37 42.6 3.8 1792 11 US-11-095-568A-1349) Sequence 38 42.6 3.8 1741 11 US-11-095-568A-1349) Sequence 38 42.6 3.8 1741 11 US-11-095-568A-1349) Sequence 40 42.2 3.8 57073 8 US-10-932-182A-79437 Sequence 41 42.2 3.8 4581 9 US-10-932-182A-79437 Sequence 42 42.2 3.8 4581 9 US-10-932-182A-79437 Sequence 42 42.2 3.8 4581 9 US-10-932-182A-79437 Sequence 42 42.2 3.8 15720 14 US-11-008-568A-1522 Sequence 52 3.7 1250 14 US-11-008-568A-1522 Sequence 52 3.7 1250 14 US-11-008-568A-1522 Sequence 52 3.7 1250 14 US-11-008-568A-1522 Sequence 52 3.7 1291 11 US-11-096-568A-1522 Sequence 62 3.7 1250 14 US-11-096-568A-12512 Sequence 63 3.7 1450 11 US-11-096-568A-1522 Sequence 64 41.8 3.7 1450 11 US-11-096-568A-12512 Sequence 64 41.8 3.7 1450 11 US-11-096-568A-12512 Sequence 64 1842, Application US/11116881A ALIGAMENTS Misser 60/665,097 PRIOR PRIDE REPRENCE: 00/665,097 PRIOR PRIDE REPRENCE: 00/665,097 PRIOR PLING DATE: 2005-03-24 PRIOR PLING DATE: 2005-03-24 PRIOR PLING DATE: 2005-03-24 PRIOR PLING DATE: 2006-03-24 PRIOR PLING DATE: 2004-09-03 PRIOR PLING DATE: 2003-09-03 PRIOR PLING DATE: 2003-0 | ţ | 0 4 | 7 T | • | 1613 | 4 - | US-11-0 | 24-959-71 | | Sequence | 71, App |
| 38 42.6 3.8 1741 11 US-11-996-568A-1349 Sequence 40 42.2 3.8 57073 8 US-10-992-182A-7947 Sequence 42.2 3.8 4581 9 US-10-932-182A-7947 Sequence 42.2 3.8 4581 9 US-10-932-182A-7947 Sequence 43 42.2 3.8 4581 9 US-10-932-182A-7947 Sequence 43 42.2 3.8 1570 14 US-11-106-568A-525 Sequence 44 41.8 3.7 1191 11 US-11-096-568A-12512 Sequence 44 41.8 3.7 1191 11 US-11-096-568A-12512 Sequence 1842, Application US/11116881A ALIGNMENTS SEQUENCE 1842, Application US/11116881A APPLICATION: NICOLEAR US/11116881A APPLICATION: NICOLEAR US/11116881A APPLICATION: NICOLEAR US/11116881A APPLICATION: NICOLEAR US/11116881A APPLICATION NUMBER: US/11/116,881A CURRENT APPLICATION NUMBER: US/11/116,881A APPLICATION NUMBER: US/65,451 PRIOR PLING DATE: 2005-04-27 PRIOR PLING DATE: 2005-03-24 PRIOR PLING DATE: 2004-09-03 PRIOR PLING DATE: 2002-10-16 PRIOR PLING DATE: 2002-10- | , | 37 | | | 1379 | 4 | US-11-0 | 96-568A-1667 | | Seguence | 16670 |
| 39 42.6 3.8 57073 8 US-10-995-561-13275 Sequence 4 42.2 3.8 4581 9 US-10-995-561-13275 Sequence 4 42.2 3.8 4581 9 US-10-932-182A-79437 Sequence 5 42.2 3.8 4581 9 US-10-932-182A-79437 Sequence 4 42.2 3.8 15720 14 US-11-108-172-1058 Sequence 5 41.8 3.7 1250 14 US-11-108-172-1058 Sequence 5 41.8 3.7 1450 11 US-11-096-568A-25694 Sequence 6 1842 A 41.8 3.7 1450 11 US-11-096-568A-12512 Sequence 1 1 US-11-096-568A-12512 Sequence 1 US-12-096-568A-12512 Sequence 1 US-12-096-598A-12512 Sequence 1 US-12-096-598A-126A-120-10-10-10-10-10-10-10-10-10-10-10-10-10 | | 38 | | | 1741 | i | US-11-0 | 96-568A-1348 | | Sequence | 13489. |
| 40 42.2 3.8 4581 9 US-10-932-182A-79477 Sequence 42 42.2 3.8 4581 9 US-10-932-182A-79477 Sequence 42 42.2 3.8 4581 9 US-10-932-182A-79477 Sequence 43 42.2 3.8 15720 14 US-11-108-172-1058 Sequence 44 41.8 3.7 1159 11 US-11-096-568A-12512 Sequence 45 41.8 3.7 1159 11 US-11-096-568A-12512 Sequence 50 US-10-095-568A-12512 Sequence 50 US-10-095-10-095-568A-12512 Sequence 50 US-10-095-1 | | 39 | | | 57073 | ω | US-10-99 | 5-561-13275 | | equence | 13275, A |
| 41 42.2 3.8 4581 9 9.2-10.24-79437 Sequence 43 42.2 3.8 4581 9 10.5-10.28-79437 Sequence 44 41.8 3.7 1191 11 US-11-086-568A-25694 Sequence 44 41.8 3.7 1191 11 US-11-096-568A-25694 Sequence 45 41.8 3.7 1191 11 US-11-096-568A-12512 Sequence 1842, Application US/11116881A ALIGNMENTS SULT 1 -11-16-881A-1842 SEQUENCE 1842, Application US/11116881A APPLICANT: Au, Dongmei APPLICANT: Nu, Dongmei APPLICANTON NUMBER: 60/665,097 PRIOR APPLICATION NUMBER: 60/665,097 PRIOR FILING DATE: 2005-03-24 PRIOR APPLICATION NUMBER: 60/666,764 PRIOR PRIIGN DATE: 2005-03-25 PRIOR APPLICATION NUMBER: 60/566,235 PRIOR PLICATION NUMBER: 60/566,235 PRIOR PLICATION NUMBER: 10/943,944 PRIOR PLICATION NUMBER: 10/943,944 PRIOR PLICATION NUMBER: 60/465,368 PRIOR PLICATION NUMBER: 60/418,933 PRIOR PLICATION NUMBER: 60/41 | | 40 | | ٠ | 4581 | σ | US-10-93 | 2-182A-79437 | | equence | 79437, A |
| 42 42.2 3.8 15720 14 US-11-1058 Sequence 44 41.8 3.7 1250 14 US-11-052-5544-532 50ULT 1 | | 41 | | • | 4581 | σ | US-10-93 | 2-182A-79437 | | equence | 79437, A |
| 43 42 550 14 US-11-096-568A-25694 Sequence 45 41.8 3.7 1191 11 US-11-096-568A-25694 Sequence 45 41.8 3.7 1191 11 US-11-096-568A-12512 Sequence 1842, Application US/11116881A PLICATION: WO. US-2006041949A1 SENERAL INFORMATION: Micelean Nucleic Acid Molecules and Uses The PRIZE OF INVERTION: Micelean Nucleic Acid Molecules and Uses The FILE REFERENCE: 07678/141014 CURRENT FILING DATE: 2005-04-27 PRIOR APPLICATION NUMBER: 60/665,097 PRIOR PLILING DATE: 2005-03-29 PRIOR FILING DATE: 2005-03-29 PRIOR PLILING DATE: 2004-09-03 PRIOR PLILING DATE: 2004-09-17 PRIOR PLILING DATE: 2004-09-18 PRIOR PLILING DATE: 2003-09-18 PRIOR PLIL | | 42 | | ٠ | 15720 | Ä | US-11-1 | 08-172-1058 | | Sequence | 1058, A |
| 44 41.8 3.7 1191 11 US-11-096-568A-12512 Sequence 1842 41.8 3.7 1450 11 US-11-096-568A-12512 Sequence 1842, Application US/11116881A 1-11-116-891A-1842 Sequence 1842, Application US/11116881A FULIANT: Nielsen, Mark T. APPLICANT: Nielsen, Mark T. TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses The FILE REFERENCE: 076-78/141014 CURRENT APPLICATION NUMBER: 05/665,057 PRIOR PELING DATE: 2005-03-24 PRIOR PELING DATE: 2005-03-24 PRIOR PILING DATE: 2005-03-24 PRIOR PELING DATE: 2005-01-25 PRIOR PELING DATE: 2005-01-25 PRIOR APPLICATION NUMBER: 60/665,097 PRIOR PILING DATE: 2006-01-35 PRIOR PELING DATE: 2004-09-03 PRIOR PELING DATE: 2004-09-03 PRIOR PILING DATE: 2003-09-18 PRIOR PILING DATE: 2003-09-18 PRIOR PILING DATE: 2003-09-10 PRIOR | υ | . 43 . 53 | 4, | ٠ | 2250 | ä | US-11-0 | 52-554A-532 | | Sequence | 532, Api |
| ALIGNMENTS SULT 1 11-116-881A-1842 Sequence 1842, Application US/11116881A Fublication No. US20060041949A1 SEQUENCE 1842, Dongmei APPLICANT: XV. Dongmei TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses The FILE REPERENCE: 07678/141014 CURRENT FILING DATE: 2005-03-24 PRIOR APPLICATION NUMBER: 60/665,451 PRIOR APPLICATION NUMBER: 60/665,097 PRIOR PILING DATE: 2005-03-24 PRIOR APPLICATION NUMBER: 60/665,097 PRIOR PILING DATE: 2005-01-25 PRIOR APPLICATION NUMBER: 60/607,357 PRIOR APPLICATION NUMBER: 60/609-03 PRIOR PILING DATE: 2004-09-03 PRIOR PILING DATE: 2004-09-03 PRIOR PILING DATE: 2004-09-03 PRIOR APPLICATION NUMBER: 60/418,933 PRIOR PILING DATE: 2003-09-18 PRIOR PILING DATE: 2003-10-16 PRIOR PILING DATE: 2003-09-18 PRIOR P | | 4 4 5 | | | 1191 | 77 | US-11-0 | 96-568A-25694 96-568A-1251 | | Sequence | 12512 |
| SQUET 1 11-116-881A-1842 Sequence 1842, Application US/11116881A Publication No. US2060041949A1 APPLICANT: Xu, Dongmei PRIOR APPLICATION NUMBER: 60/665,451 PRIOR APPLICATION NUMBER: 60/665,097 PRIOR PILING DATE: 2005-03-24 PRIOR PILING DATE: 2006-03-36 PRIOR PILING DATE: 2004-09-03 PRIOR PLING DATE: 2004-09-03 PRIOR PLING DATE: 2004-09-03 PRIOR PPLING DATE: 2004-09-03 PRIOR PLING DATE: 2004-09-17 PRIOR PLING DATE: 2004-09-17 PRIOR PLING DATE: 2004-09-17 PRIOR PLING DATE: 2003-09-18 PRIOR PLING DATE: 2004-0 | | | | | | | ALLGN | AEN I S | | | |
| -11-16-881A-1842 Fequence 1842, Application US/11116881A Fequence 1842, Application US/11116881A Fequence 1843, Application US/11116881A FEQUENCE OF UNCORMATION: APPLICANT: Nu, Dongmei FILE REFERENCE: 076-14101 FILE REFERENCE: 076-14101 FILE REPERENCE: 076-16101 FILE R | REST | ULT 1 | | | | | | | | | |
| Acid Molecules 881A 8d - See File W | us-: | 11-116 | -881A-1 | 1842 | 107 | , | **** | | | | |
| Rcid Molecules 881A 861 - See File W | ň 6 | equence | e 1842, | Appli | cation | US/1 | 1116881A | | | | |
| PPLICANT: Xu, Dongmei PPLICANT: Xu, Dongmei TILE OF INVENTION: Nicotiana Nucleic Acid Molecules ILE REFERENCE: 07678/141014 URRENT APPLICATION NUMBER: US/11/116,881A URRENT PILING DATE: 2005-04-27 RIOR PPLICATION NUMBER: 60/665,451 RIOR PPLICATION NUMBER: 60/665,451 RIOR FILING DATE: 2005-03-24 RIOR FILING DATE: 2005-03-24 RIOR FILING DATE: 2005-03-24 RIOR FILING DATE: 2005-03-25 RIOR FILING DATE: 2004-09-03 RIOR FILING DATE: 2004-09-17 RIOR PPLICATION NUMBER: 60/566,235 RIOR FILING DATE: 2004-09-17 RIOR PPLICATION NUMBER: 60/603,368 RIOR FILING DATE: 2003-09-18 RIOR RELING DATE: 2003-09-18 RIOR RELING DATE: 2003-09-18 RIOR APPLICATION NUMBER: 60/418,933 RIOR RELING DATE: 2003-09-18 RIOR APPLICATION NUMBER: 60/418,933 RIOR RELING DATE: 2003-07-08 RIOR APPLICATION NUMBER: 60/418,933 RIOR RELING DATE: 2003-07-08 RIOR RELING DATE: 2003-07-08 | ¥ 6 | SNERAL | INFORM | AATTON: | 00004TA | 4 9 A I | | | | | |
| PPLICANT: Nielsen Mark T. TILE OF INVENTION: Nicotiana Nucleic Acid Molecules ILIE REPERRUGE: 07678/141014 URRENT APPLICATION NUMBER: US/11/116,881A URRENT FILING DATE: 2005-04-27 RIOR APPLICATION NUMBER: 60/665,451 RIOR APPLICATION NUMBER: 60/665,097 RIOR FILING DATE: 2005-01-24 RIOR FILING DATE: 2005-01-25 RIOR FILING DATE: 2005-01-25 RIOR FILING DATE: 2004-09-03 RIOR RILING DATE: 2004-09-17 RIOR FILING DATE: 2004-09-18 RIOR FILING DATE: 2004-09-18 RIOR FILING DATE: 2003-09-18 RIOR FILING DATE: 2003-09-18 RIOR RILING DATE: 2003-09-10-10-10-10-10-10-10-10-10-10-10-10-10- | | APPLICA | ANT: Xu | 1, Dong | mei | | | | | | |
| ILIE DE INVENTION: Nicotiana Nucleic Acid Molecules ILIRE REFERENCE: 10578/141014 URRENT APPLICATION NUMBER: US/11/116,881A URRENT FILING DATE: 2005-04-27 RIOR APPLICATION NUMBER: 60/665,451 RIOR PILING DATE: 2005-03-24 RIOR PILING DATE: 2005-03-24 RIOR PILING DATE: 2005-01-25 RIOR PELICATION NUMBER: 60/646,764 RIOR FILING DATE: 2004-09-03 RIOR PILING DATE: 2004-09-18 RIOR PILING DATE: 2004-09-18 RIOR RILING DATE: 2003-09-18 RIOR PILING DATE: 2003-09-18 RIOR RILING DATE: 2003-09-18 RILING DATE: 2003-09-18 RILING DATE: 2003-09-18 RILING PAPELICATION NUMBER: 60/488,338 RICH RILING DATE: 2003-09-18 RILING DATE: 2003-09- | | APPLIC? | ANT: N | Vielsen | 1, Mark | ₽. | | | | | |
| THE REFERENCE: 0.0 80/11/116,881A URRENT APPLICATION NUMBER: 00/665,451 RIOR APPLICATION NUMBER: 60/665,451 RIOR APPLICATION NUMBER: 60/665,451 RIOR FILING DATE: 2005-03-24 RIOR PILING DATE: 2005-03-24 RIOR APPLICATION NUMBER: 60/646,764 RIOR FILING DATE: 2005-01-25 RIOR APPLICATION NUMBER: 60/646,764 RIOR FILING DATE: 2004-09-03 RIOR PILING DATE: 2004-09-18 RIOR PILING DATE: 2003-09-18 RIOR PILING DATE: 2003-09-18 RIOR RILING DATE: 2003-0 | | TITLE (| JANI JO | ENTION: | Nicoti | ana | Nucleic 1 | Acid Molecule | | Uses Ther | .eof |
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APPLICANT: Xu, Dongmei
APPLICANT: Nielsen, Mark T.
ITILE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REPERBNCE: 07678/14101E
CURRENT APPLICATION NUMBER: US/11/116,881A
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PRIOR APPLICATION NUMBER: 60/566,235
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Publication No. US20060041949A1
GENERAL INFORMATION:
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TITLE OF TUTZENTON: Nicociana Nucleic Acid Molecules and Uses Thereof

TILE OF TUTZENTON: Nicociana Nucleic Acid Molecules and Uses Thereof

TILE OF TUTZENTON: NICOCIANA

CURRENT APPLICATION NUMBER: US/11/116,881A

CURRENT PILING DATE: 2005-03-24

PRIOR FILING DATE: 2005-03-24

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PRIOR APPLICATION NUMBER: 60/646,764

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                                   Indels
   al Similarity 53.9%; Pred. No. 2.1e-14; 200; Conservative 0; Mismatches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1704, Application US/11116881A Publication No. US20060041949A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn version 3.3
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Best Local Similarity
Matches 200; Conserv
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SEQ ID NO 1704
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                                                                                                                                                                                                                                                                                                                                                                                                                                   277 GGGGCACACGTGCACCTTTACTCGTTAACATTTACCCCTATTTCAGCTATTCTGGTAATC 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 1232, Application US/11116881A
| Sequence 1232, Application US/11116881A
| Publication No. US20060041949A1
| GENERAL INFORMATION:
| APPLICANT: Xu, Dongmei
| APPLICANT: Xu, Dongmei
| APPLICANT: Nielsen, Mark T.
| TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
| FILE REFREENCE: 07678/141014
| CURRENT APPLICATION NUMBER: US/11/116,881A
| CURRENT PILING DATE: 2005-04-27
| PRIOR APPLICATION NUMBER: 60/665,097
| PRIOR APPLICATION NUMBER: 60/665,097
| PRIOR FILING DATE: 2005-01-25
| PRIOR FILING DATE: 2006-01-25
| PRIOR FILING DATE: 2004-09-03
| PRIOR FILING DATE: 2003-09-18
| PRIOR FILING DATE: 2003-09-18
| PRIOR PILING DATE: 2003-09-18
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                                                                                                                    AGAACATCAAGGTCTCCACATCAGTCTCCTTCGGCGTCGTCGGTACCTCATATCCCCCCT
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                    Pred. No. 6.9e-13;
0; Mismatches 87; Indels
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                    60.5%;
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                                                Matches 133; Conservative
                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        131 CCGCCGACGTCGTCAACCTCTACAAGTCCAACATAGCTGGCATGCGACTCTACAGCC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                      160 ATTGGGAAGTTATACAGCTCTACAAGTCAAGAACATAGGAAGACTGAGGCTTTATGATC 219
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                                                                                                       11 CTCAGCACATCATCCCATGGCTGCCATGGCATCCCTTGTAGTACTCTCGGCAATCC 70
                                                                                                                                                                 40 crccrchahregerecraracaerceraeahrachaeirachierreceaeaeaerreaea 99
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Publication No. US20060041949A1

Fublication No. US20060041949A1

Fublication No. US20060041949A1

APPLICANT: Xu, Dongmei

APPLICANT: Xu, Dongmei

APPLICANT: Xu, Dongmei

APPLICANT: Nielsen, Mark T.

TITLE OF INVENTION: NICOLIAIRA NUCleic Acid Molecules and Uses Thereof

FILE REFERENCE: 07678141014

CURRENT APPLICATION NUMBER: 06/65,451

FRIOR PILING DATE: 2005-03-24

FRIOR FILING DATE: 2005-03-24

FRIOR FILING DATE: 2005-03-24

FRIOR FILING DATE: 2005-01-25

FRIOR PILING DATE: 2004-09-03

FRIOR FILING DATE: 2003-07-08

FRIOR FILING DATE: 2003-07-08
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Best Local Similarity 53.9%; Pred. No. 2.2e-14;
Matches 200; Conservative 0; Mismatches 168; Indels
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SEQ ID NO 703
LENGTH: 386
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US-11-116-881A-703
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US-11-116-881A-703
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Sequence 517, Application US/11052554A

Publication No. US20050288866A1

GENERAL INFORMATION:

APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REPRESENCE: 30653/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT APPLICATION NUMBER: US 00/5-02-07

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE PATENTIN VETSION 3.3

SEQ ID NO 517

LENGTH: 9903
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Publication No. US2055278800A1

GENERAL INFORMATION:

APPLICANT: Blenner, Claire

APPLICANT: Hall, Claire

APPLICANT: Demmer, Jeroen

TITLE OF INVENTION: Genme expression.

FILE REPRENCE: 11001.1086U

CURRENT PILNG DATE: 2005-05-25

PRIOR APPLICATION NUMBER: 60/580,007

PRIOR PILING DATE: 2004-06-15

NUMBER OF SEQ ID NOS: 66

SOFTWARE FRACES FRACES

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 16

LENGTH: 1501
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Similarity 50.3%; Pred. No. 7.6e-05;
52; Conservative 0; Mismatches 157;
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US-11-052-554A-517
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US-11-138-987-16/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 ACCTCTACAAGACCAAGACATAGCTGGCATGCGACTCTACAGCCCGACCAAGCCACTC 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 GCCCCTACTCCGTCCTCGTCTTCGACGCCACCTCGCTCCACTCCAAGACCCGACCTCC 286
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228 AGATACAAATGTCTTCAACGCTCTCAGAGGAAGTAACATTGAGATCATTCTCGACGTCCC 287
                                                                           CAACTCCGACCTCCAAAACATTGCCTCCGACCAATCCGCCGCCACCAACTGGGTCCAAAC 311
                                                                                                                        288 ACTICAAGAICTICAAICCCIAACIGAICCTICAAGAGCCAAIGGAIGGGICCAAGAIAA 347
                                                                                                                                                                        CAACGICCAAGCCIACCCAAACGIIGCCIICCGAIACAICGCCGICGGAAACGAAGTCAI 371
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45.6%; Pred. No. 2e-05;
tive 0; Mismatches 234; Indels 0;
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; OTHER INFORMATION: Ceres Seq. ID no. 15179743
US-11-096-568A-9277
                                                                                                                                                                                                                                                                                                                     408 TCCCGGAAATAATGGTCAATATG 430
                                                                                                                                                                                                                                                                        CCCCGGCGGCCAAGCTCAGTACG 394
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Matches 196, Conservative
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APPLICANT: Charlebois, Timothy S.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Binacore, Martin S.
APPLICANT: Broand, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miler, Christopher P.
TITLE OF INVENTION: NOWEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: NOWEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: NOWEL POLYNUCLEOTIDE ARRAYS
TITLE OF INVENTION: OWNITOR GENE EXPRESSION
FILE REPERENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT APPLICATION NUMBER: US/60/570,425
PRIOR APPLICATION NUMBER: US/60/570,425
PRIOR PILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: Patentin version 3.3
SEQ ID NO 426
LENGTH: 6645
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                                                                                                                                                                                                                                                                   520 CTCTCTTTCTCACAAAGACACCACTCTCTTTTTTGTGACAATCTCTCCTTTCTAAGC 461
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                                                                                                                                                         493 TCATATCCCCCCTCAGCTGGCTCCTTCTTCCGATGCATCGTCGACATTGGGTCCAATC
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                                                                            Score 49.6; DB 14; Length 1501;
Pred. No. 0.0011;
0; Mismatches 229; Indels 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 426, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Arabidopeis thaliana
US-11-138-987-16
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J. OTHER INFORMATION: n is a, c, US-11-128-061-426
                                                                          Query Match
Best Local Similarity 47.5%;
Matches 213; Conservative
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APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Martin S.
APPLICANT: Sinacore, Martin S.
APPLICANT: Branch, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR TITLE OF INVENTION: MAKING AND USING SAME FILE REFERENCE: 01997.027700
CURRENT APPLICATION WINBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
PRIOR FILING DATE: 2004-05-11
                                                                                                                                                                                                                                                                                                                                                                              5121 dadccacecrccccadagecraracacccagaeccrrcaracrcrcracracraccy 5180
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                                                                                                              GTGACAACCTCCCCCAGCCCGCCGACGTCGACCTCTACAAGTCCAACAACATAGCTG 172
                                                                                                                                                                                                                                                                                                                                          233 ACCTCATCCTCGACGTCCCCAACTCCGACCTCCAAAACATTGCCTCCGACCAATCCGCCG
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                                                           Gaps
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4.3%; Score 48.2; DB 14; Length 6645;
41.7%; Pred. No. 0.0051;
ive 24; Mismatches 252; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
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SEQ ID NO 426
LENGTH: 6645
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i LOCATION: (4002)...(4019)
i OTHER INFORMATION: n is a,
US-11-128-049-426
                       Best Local Similarity 41.7
Matches 204; Conservative
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649 ACAACT---TCTACAACTTCTACCACTCCTACAACTTCTACCACTCCTACAACTTCTACA 705
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   529 TCTACCACTCCTACAACTTCTACCACATCGACTACTCCTACAACCTCTACTACTACTACC 588
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                                                                  TCATCCTCGACGTCCCCAACTCCGACCTCCAAAACATTGCCTCCGACCAATCCGCCGCCGCA
                                                                                                                                                                                             296 CCAACTGGGTCCAAACCAACGTCCAAGCCTACCCAAACGTTGCCTTCCGATACATCGCCG
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                                                                                                                              589 ACTCCTACAACTICTACCACATCGACTACTCCTACAACCTCTACTACTTCTACCACTCCT
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, TOMOKO
APPLICANT: KUJIMURA, TOMOKO
TITLE OP INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT PILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SCPTWARE: Patentin version 3.3
SEQ ID NO 191019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 TOGGCGTCGTCGTACCTCATATCCCCCTCAGCTGGCTCCTTCTCTTCCGA
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Pred. No. 0.0077;
0; Mismatches 218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Saccharomyces pastorianus
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US-10-932-182A-191019
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                                                                                                                              GTGACAACCICCCCAGCCCGCCGACGTCGTCAACCTCTACAAGTCCAACAACATAGCTG 172
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Sequence 191019, Application US/10932182A
Publication No. US20060046253A1
GENERAL INPORANTION:
APPLICANT: NAKAMURA, NORIHIRO
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: REFERENCE: OSO685-043
CURRENT APPLICANTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOPTWARE: Patentin version 3.3
SOPTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 CGTCGACATTGGGTCCAATCATACAGTTTCTAGCCAGCAATGGCTCCCCATTACTTGCCA
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4.3%; Score 48.2; DB 14; Length 41.7%; Pred. No. 0.0051; ive 24; Mismatches 252; Indels
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; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-191019
                                                               204; Conservative
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                                 Similarity
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Best Local S
Matches 204
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Publication No. US2050287641A1

Publication No. US2050287641A1

APPLICANT: Farnet, Chris

APPLICANT: Zazopoulos, Emmanuel

APPLICANT: Zazopoulos, Emmanuel

APPLICANT: Graffa, Alfredo

TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS

FILE REFERENCE: 3002-2US

CURRENT APPLICATION NUMBER: US/11/205,109

CURRENT FILING DATE: 2005-08-17

PRIOR APPLICATION NUMBER: US/09/976,059

PRIOR FILING DATE: 2001-10-15

PRIOR FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin version 3.0
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LOCATION: (15591)..(15863)
OTHER INFORMATION: ORF 11; positive strandedness
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LOCATION: (15203)..(13614)
OTHER INFORMATION: ORF 10; negative strandedness
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LOCATION: (2077)..(3078)
OTHER INFORMATION: ORF 1; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRATURE:
NAME/KEY: misc feature
LOCATION: (3118)..(4032)
OTHER INFORMATION: ORF 2; positive strandedness
PEATURE:
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LOCATION: (4038)..(5048)
OTHER INFORWATION: ORF 3; positive strandedness
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LOCATION: (6665)..(5814)
OTHER INFORMATION: ORF 4; negative strandedness
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LOCATION: (7703)..(6693)
OTHER INFORMATION: ORF 5; negative strandedness
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LOCATION: (9464)..(8130)
OTHER INFORMATION: ORF 6; negative strandedness
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LOCATION: (9691)..(10761)
OTHER INFORWATION: ORF 7; positive strandedness
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LOCATION: (12751)..(10829)
OTHER INFORMATION: ORF 8; negative strandedness
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LOCATION: (13617)..(12802)
OTHER INFORWATION: ORF 9; negative strandedness
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LENGTH: 88421
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NAME/KEY: misc feature

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NAME/KEY: misc_feature
LOCATION: (39713)..(65800)
OTHER_INFORMATION: ORF 14; positive strandedness
LOCATION: (15880)..(19035)
OTHER INFORMATION: ORP 12; positive strandedness
PRATURE:
                                                                               NAME/KEY: misc_feature
LOCATION: (19032)..(39713)
OTHER INFORMATION: ORF 13; positive strandedness
FRATURE:
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LOCATION: (65826)..(66530)
OTHER INFORMATION: ORF 15; positive strandedness
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NAME/KEY: misc_feature
LOCATION: (66546)..(67370)
OTHER INFORMATION: ORF 16; positive strandedness
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LOCATION: (73439)..(71964)
OTHER INFORMATION: ORF 20; negative strandedness
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LOCATION: (70099)..(70662)
OTHER INFORMATION: ORF 18; positive strandedness
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LOCATION: (74216)..(73563)
OTHER INFORMATION: ORF 21; negative strandedness
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LOCATION: (79864)..(78107)
OTHER INFORMATION: ORF 25; negative strandedness
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LOCATION: (67384)..(70059)
OTHER INFORMATION: ORF 17; positive strandedness
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LOCATION: (70659)..(71906)
OTHER INFORMATION: ORF 19; positive strandedness
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LOCATION: (75424)..(74213)
OTHER INFORMATION: ORF 22; negative strandedness
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LOCATION: (75535)..(76464)
OTHER INFORMATION: ORF 23; positive strandedness
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LOCATION: (78110)..(76449)
OTHER INFORMATION: ORF 24; negative strandedness
FRATURE:
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LOCATION: (81624)..(79861)
OTHER INFORMATION: ORF 26; negative strandedness
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LOCATION: (81909)..(81682)
OTHER INFORMATION: ORF 27; negative strandedness
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LOCATION: (82346)..(82062)
OTHER INFORMATION: ORF 28; negative strandedness
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LOCATION: (82587)..(84446)
OTHER INFORMATION: ORF 29; positive strandedness
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NAME/KEY: misc_feature
LOCATION: (84481)..(85548)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52991 GCCGACCACCCCCGTCCCGCCGAGGCCACCTACCGCGGCCACACCGTGGAGTTCACCGTG 53050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53111 ATGACCGTGCAAACCGCCCTCGCCGTCCTGTCCAAACTCGGCGCCGGCACCACATC 53170
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                                                                                                                                                                                                                                                                                                                                                                                                                           115 GACAACCTCCCCCAGCCCGCCGACGTCGTCAACCTCTACAAGTCCAACATAGCTGGC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 ATGCGACTCTACAGCCCCGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAACATCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Appl#cation US/11121086
Publication No. US20050266459A1
Sequence 42, Appl#cation WS/11121086
Publication No. US20050266459A1
APPLICANT: INFORMATION:
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, WUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-000000
CURRENT APPLICATION NUMBER: 105/11/121,086
CURRENT FILING DATE: 2005-05-04
RIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE PARENT PLANCE AND NOS: 107
SOFTWARE PARENT PLANCE AND NOS: 107
SOFTWARE PARENT PLANCE AND NOS: 107
SOFTWARE PARENT NOS: 107
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                           FEATURE:

NAME/KEY: misc_feature

LOCATION: (87454)..(88420)

OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-11-205-109-1
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                                                                                                                                                                                                                                                                                                                                   Score 47.2; DB 14; Length 88421;
Pred. No. 0.028;
0; Mismatches 173; Indels 0;
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Pred. No. 0.039;
0; Mismatches 145; Indels 0;
OTHER INFORMATION: ORF 30; positive strandedness
                                                              LOCATION: (85556)..(86845)
OTHER INFORMATION: ORF 31; positive strandedness FRATURE:
NAME/KYS: misc feature
LOCATION: (87372)..(86803)
OTHER INFORMATION: ORF 32; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53291 crecaccecaccecacacaccace 53314
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Best Local Similarity 46.6%;
Matches 151; Conservative (
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Best Local Similarity 48.0%;
Matches 134; Conservative
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; ORGANISM: Homo sapiens
US-11-121-086-42
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US-11-121-086-42
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131645 CTTATCTCTATCTATCTACACCCCATCCACATCTCCATCACTACAACCTCATCCTATC 131704
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22727 TCCATCATATACAACTCCATCCTCATCTCCAAAACATACAACCCCATCCCCACCTCCATC 22786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WU, RINA
APPLICANT: WAGUEZ, ABBEY
TITLE OF INVENTION: CRROWGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 0618.011.0004
CURRENT PEPLICATION NUMBER: US/11/114,798
CURRENT PELLING DATE: 2005-04-26
PRIOR APPLICATION NUMBER: 10/173,525
PRIOR APPLICATION NUMBER: 09/952,851
PRIOR PLILING DATE: 2002-06-17
PRIOR PLILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PALENTIN OF: 3.3
                                                                                                                                                                                                           277 TCCGACCAATCCGCCGCCACCAACTGGGTCCAAACCAACGTCCAAGCCTACCCAAACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131585 céchréccégerréchréndendandecéntécédacérechréndandené
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                                                                              217 CAGGGCTCTAACATCTACCTCATCCTCGACGTCCCCAACTCCCGACCTCCCAAAACATTGCC
                                                                                                                                         22667 cerarererareareracecearecaererererearearacarecreare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: nucleotide sequence
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Pred. No. 0.042;
0; Mismatches 145; Indels
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                                                                                                                                                                                                                                                                                                                                                                                             22787 Acatachaccccatrcccarcarcardachaccc 22825
                                                                                                                                                                                                                                                                                                                                        337 GCCTTCCGATACATCGCCGTCGGAAACGAAGTCATCCCC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 GCCTTCCGATACATCGCCGTCGGAAACGAAGTCATCCCC 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 52, Application US/11114798; Publication No. US20060035246A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 48.0%;
Matches 134; Conservative (
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SEQ ID NO 52
LENGTH: 165911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-114-798-52
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